

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 18.9198 Seconds
(without alignments)
620.432 Million cell updates/sec

Title: US-10-092-934-2
Perfect score: 651
Sequence: 1 MMVCNRFKQWVFISAIFN.....RNTIDQQLSRILKIKRL 122

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	13.5	282	2 B71227	hypothetical prote
2	77.5	11.9	401	2 S42583	phosphate transloc
3	77	11.8	280	2 H75194	hypothetical prote
4	76.5	11.8	1132	2 T45037	hypothetical prote
5	73	11.2	483	2 S45347	probable G protein
6	72.5	11.1	414	2 S34829	triose phosphate/3
7	71.5	11.0	392	2 D83934	hypothetical prote
8	71.5	11.0	798	2 H81040	penicillin-binding
9	71	10.9	244	2 F69260	nitrate ABC transp
10	70.5	10.8	672	2 C69120	conserved hypotet
11	70	10.8	409	2 S37497	triose phosphate/3
12	70	10.8	855	2 E90106	importin beta-1 su
13	69.5	10.7	148	2 S58751	NADH2 dehydrogenas
14	69	10.6	205	2 G84994	cytochrome o ubiqu
15	68.5	10.5	297	2 H89103	protein C18B10.1 [
16	68.5	10.5	414	2 S23224	triose phosphate/3
17	68	10.4	171	2 T28384	ORF MSV223 hypote
18	67.5	10.4	228	2 H36950	ureH protein - Bac
19	67	10.3	175	2 S57903	probable amino aci
20	67	10.3	182	2 S74646	spore maturation p
21	67	10.3	515	2 S53525	G protein-coupled
22	67	10.3	793	2 S68228	trp-1 protein - hu
23	66.5	10.2	360	2 E88922	protein W03F9.6 [1
24	66.5	10.2	1353	2 S26301	hypothetical prote
25	66	10.1	677	2 S32816	potassium channel
26	65.5	10.1	348	2 S18521	pheromone p-factor
27	65.5	10.1	582	2 S38184	hypothetical prote
28	65	10.0	250	2 T31835	hypothetical prote
29	65	10.0	263	2 A12384	hypothetical prote

30	65	10.0	297	2 T27206	hypothetical prote
31	65	10.0	373	2 D81286	probable integral
32	65	10.0	537	2 T26800	hypothetical prote
33	65	10.0	622	2 G81981	probable lipopolys
34	65	10.0	622	2 B71326	probable V-type AT
35	65	10.0	623	2 B81037	lipopolysaccharide
36	65	10.0	628	2 A99317	conserved hypotet
37	65	10.0	846	2 T19179	hypothetical prote
38	64.5	9.9	280	2 T33268	hypothetical prote
39	64.5	9.9	304	2 AD0864	probable membrane
40	64.5	9.9	478	2 T29174	hypothetical prote
41	64.5	9.9	558	2 C96790	hypothetical prote
42	64.5	9.9	586	2 AE0786	probable sulphatas
43	64.5	9.9	655	2 A12556	hypothetical prote
44	64	9.8	186	1 D69206	conserved hypotet
45	64	9.8	468	2 AD0521	probable symporter

ALIGNMENTS

RESULT 1

B71227
hypothetical protein PH0076 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: B71227
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: B71227
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-282 <KAW>
A:Cross-references: UNIPROT:O57787; GB:AP000001; NID:G3236128; PIDN:BAA29145.1; PID:G325
A:Experimental source: strain OT3
A>Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0076

Query Match	13.5%	Score 88;	DB 2;	Length 282;
Best Local Similarity	27.4%;	Pred. No. 0.03;		
Matches	31;	Conservative	16;	Mismatches 42; Indels 24; Gaps 6;
Qy	6	NRFCKWVYFISAIFNFGPRVLYHGVFYFLIVRIISFLI--GDMEVDLLNCTLLKRSSR	63	
Db	73	NOYETWQFFRSIIFTMAA-----FFLLASVLSFYVFFGKKRYVIFK--VVSEAKL	120	
Qy	64	FRFWGALVCSMDCRSRFRVAVTVRFITLLNIPSPAVMARNITDQQLSRILK	116	
Db	121	SKLMGAYCYCDRNSC---YAV---FKALLNARLPGIAIAR---DPPEIFREKL	163	

RESULT 2

S42583
phosphate translocator, chloroplast - common tobacco
N:Alternate names: triose phosphate/3-phosphoglycerate/phosphate translocator
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S42583; S37224
R:Knight, J.S.; Gray, J.C.
Mol. Gen. Genet. 242, 586-594, 1994
A:Title: Expression of genes encoding the tobacco chloroplast phosphate translocator is
A:Reference number: S42583; MUID:94166771; PMID:8121415
A:Accession: S42583
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-401 <KNI>
A:Cross-references: UNIPROT:Q40568; EMBL:X75088; NID:G403022; PIDN:CAA52979.1; PID:G4030
C:Superfamily: triose phosphate/3-phosphoglycerate/phosphate translocator
C:Keywords: chloroplast

QY 59 KRSSRFPGALVCSMDSCRSFSAVVTY-----RFITLLNIPSPAVWMA 102
Db 175 KLLTPVAFCHALGHVTSNAAFAVRVSFTTHVKALEBFFNAAASQFILGQOIPU-ALWLS 233

RESULT 7
D83934
hypothetical protein BH2276 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: D83934
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83934
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-392 <SFO>
A;Cross-references: UNIPROT:Q9KAL1; GB:AP001515; GB:BA000004; NID:gl0174886; PIDN:BAR059
C;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2276

Query Match 11.0%; Score 71.5; DB 2; Length 392;
Best Local Similarity 26.8%; Pred. No. 3;
Matches 33; Conservative 18; Mismatches 47; Indels 25; Gaps 6;

QY 15 ISALFNFGPRYLHGVPFYFLILVRIISFL-----IGMEDVLLNCTLLKRSSRF---RF 66
Db 82 IVAIFAFMGAASFAG---YIFMFEVLFLSPPTALGDS---LAQKTAINRRLSFGKIRM 135

QY 67 WGAIVCSMDSCR-----FSRVAVTYRFTITLNIIPSPAVWM-----ARNTIDQQVLSRIK 115
Db 136 WGSGLGFTSLAVGYILAAIGVTVIMVPLVTVISLWLSRGLBDFDFTTKPVTLLSALK 195

QY 116 LEI 118
Db 196 LAI 198

RESULT 8
H81040
penicillin-binding protein 1 NMB1807 [imported] - Neisseria meningitidis (strain MC58 se
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: H81040; F81985
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: H81040
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-798 <TT>
A;Cross-references: UNIPROT:O05194; GB:AE002530; GB:AE002098; NID:g7227054; PIDN:AAF4214
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: F81985
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-798 <PAR>
A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83943.1; PID:g737938
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: ponA; NMB1807; NMA0655

C;Superfamily: penicillin-binding protein

Query Match 11.0%; Score 71.5; DB 2; Length 798;
Best Local Similarity 31.2%; Pred. No. 6.4;
Matches 24; Conservative 9; Mismatches 31; Indels 13; Gaps 3;

QY 45 IGMEDVLLNCTLLKRSSF-RFWGALVCSMDSCRSFSAVVTYRFTITLLNIPSPAVWMAR 103
Db 73 IGFPFVLRNAVTAEDKRFYRHG-----VDVMGVARAAVG-----NVVSGSQSGA 120
QY 104 NTIDQQVLSRIKLEIKR 120
Db 121 STITQQVAKNFYLSSEK 137

RESULT 9
F69260
nitrate ABC transporter, permease protein (nrtB-1) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: F69260
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: F69260
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-244 <KLE>
A;Cross-references: UNIPROT:O30150; GB:AE001100; GB:AE000782; NID:g2689423; PIDN:AAB9114
C;Superfamily: Synechococcus nitrate transport protein nrtB

Query Match 10.9%; Score 71; DB 2; Length 244;
Best Local Similarity 25.6%; Pred. No. 2.1;
Matches 23; Conservative 22; Mismatches 35; Indels 10; Gaps 2;

QY 25 YLVHGVPFYFLILVRIISFLIGMEDVLLNCTLLKRSSRFPGALVCSMDSCRSFSAV 84
Db 93 YLLVPIPHIVLLPLYILLFGDLSRVLLIATIL-----FFQIAVTRDA---AKQVS 142

QY 85 TYRFTITLLNIPSPAVWMARNTIDQQVLSRI 114
Db 143 DYYVYSILSGASKIDIYRHIIPAVMPKI 172

RESULT 10
C69120
conserved hypothetical protein MTH1898 - Methanobacterium thermoautotrophicum (strain De
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69120
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Viclaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: C69120
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-672 <MTH>
A;Cross-references: UNIPROT:O27920; GB:AE000941; GB:AE000666; NID:g2623025; PIDN:AAB8635
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1898
A;Start codon: TTG

Query Match 10.8%; Score 70.5; DB 2; Length 672;
Best Local Similarity 27.5%; Pred. No. 6.9;

C;Accession: H89103
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2103, 1999; and
A;Accession: H89103
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-297 <STO>
A;Cross-references: UNIPROT:P91077; GB:chr_V; PIDN:AAC25812.1; PID:g3294493; GSPDB:GN000000000
C;Genetics:
A;Gene: C18810.1
A;Map position: 5

Query Match 10.5%; Score 68.5; DB 2; Length 297;
Best Local Similarity 30.4%; Pred. No. 4.9;
Matches 21; Conservative 18; Mismatches 19; Indels 11; Gaps 3;
Qy 36 ILVRIISFLIGDMEDVLL--NCTLLKSSRRFRFWGALVCSMDSCRFS-----RVAVT 85
Db 136 VIVLILAIISLGTLENLVLFQSC-LNLSNIPKNGVLRCAVDACFFSYWASDRSAMPALN 194
Qy 86 YRFITLNI 94
Db 195 FIFGGLLSI 203

Search completed: October 11, 2005, 07:01:32
Job time : 21.9198 secs

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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 73.2326 Seconds
(without alignments)
853.085 Million cell updates/sec

Title: US-10-092-934-2
Perfect score: 651
Sequence: 1 MMVCWRNRFQKWWYFSAIFN.....RNTIDQQVLSRIKLEIKRCL 122

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	13.5	282	2	Q57787 pyrococcus
2	79.5	12.2	417	2	Q9FTT3 oryza sativ
3	78	12.0	417	2	Q9ARH5 oryza sativ
4	77.5	11.9	401	2	Q40568 nicotiana t
5	77	11.8	280	2	Q9V2J1 pyrococcus
6	76.5	11.8	265	2	Q8MYN2 caenorhabdi
7	75	11.5	295	2	Q8PS42 methanosarc
8	75	11.5	402	2	Q9ATY2 triticum ae
9	74.5	11.4	178	2	Q8IF34 trypanosoma
10	74.5	11.4	320	2	Q8LA34 arabidopsis
11	74.5	11.4	380	2	Q75FMI leptospira
12	74.5	11.4	380	2	Q8EXK4 leptospira
13	74.5	11.4	449	2	Q8W47 lactobacill
14	74.5	11.4	462	2	Q7R1C2 giardia lam
15	74	11.4	347	1	Q8SV_XENLA
16	73.5	11.3	515	2	Q8OWT4 mus musculu
17	73	11.2	463	2	Q8G4Y8 bifidobacte
18	73	11.2	483	2	Q64017 rattus sp.
19	72.5	11.1	268	2	Q97C97 thermoplas
20	72.5	11.1	384	2	Q8Z40 pyrobaculum
21	72.5	11.1	790	2	Q6DHES brachydanio
22	72	11.1	292	2	Q6CS38 kluyveromyc
23	72	11.1	447	2	Q63231 rattus norv
24	72	11.1	1008	2	Q9VQZ8 drosophila
25	71.5	11.0	392	2	Q9KAL1 bacillus ha
26	71.5	11.0	394	2	Q8Z49 pyrobaculum
27	71.5	11.0	797	1	Q5131 neisseria g
28	71.5	11.0	798	1	Q5194 neisseria m
29	71.5	11.0	1278	2	Q9U8G3 onchocera
30	71	10.9	244	2	O30150 archaeoglob
31	71	10.9	783	1	Q9W799 xenopus lae

32 70.5 10.8 314 2 Q8E427 streptococc
33 70.5 10.8 672 2 Q27920 methanobact
34 70 10.8 394 2 Q6VV64 mus musculu
35 70 10.8 409 1 CPTP_MAIZE
36 70 10.8 492 2 Q83E30
37 70 10.8 581 2 Q6CUT8 kluyveromyc
38 70 10.8 634 2 Q8S298 oryza sativ
39 70 10.8 855 2 Q9AW68 guillardia
40 70 10.8 1564 2 Q8ISW4 plasmodium
41 69.5 10.7 148 1 NU3M_HANWI
42 69 10.6 205 1 CYOC_BUCAI
43 69 10.6 353 2 Q6FTC4 buchnera ap
44 69 10.6 421 2 Q98IA5 rhizobium l
45 68.5 10.5 297 2 P91077 caenorhabdi

ALIGNMENTS

RESULT 1

O57787 ID O57787 PRELIMINARY; PRT; 282 AA.
AC O57787;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein PH0076.
GN OrderedLocusNames=PH0076;
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Mauchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL; AP000001; BAA29145.1; -.
DR PIR; B71227; B71227.
DR InterPro; IPR008553; DUF835.
DR Pfam; PF05763; DUF835; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 282 AA; 32359 MW; C960845D3B178747 CRC64;

Query Match 13.5%; Score 88; DB 2; Length 282;
Best Local Similarity 27.4%; Pred. No. 0.34;
Matches 31; Conservative 16; Mismatches 42; Indels 24; Gaps 6;

Oy 6 NREKQWYFSAIFNFGPRVLYHGVFYLVRISFLI--GMEDVLLNCTLLKSSR 63
Db 73 NQYETWQFFRSIFLFTMAA-----FFLLASVLSFYVFGKKRYVFK--VVSEAKL 120
Oy 64 FRFWGALVCSMDSCRSRVAVYRFTILLNIPSPAVMARNITDQVLSRIKL 116
Db 121 SKLWGAYCYDRNSC----YAV---FKALLNARLPGIAIAR---DPPEIFREKL 163

RESULT 2

O9FTT3 ID O9FTT3 PRELIMINARY; PRT; 417 AA.
AC O9FTT3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative triose phosphate/phosphate translocator.

GN Name=OSJNBa0086P08.23; Synonyms=OSJNBa0010K01.4;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Erihartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12474738; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijiishi S., Honda M., Ichikawa Y., Ikonuma A., Iijima M., Ikeda M.,
RA Ikeno M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi T., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagaaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP002855; BAB17213.1; -
DR EMBL; AP003210; BAB40092.1; -
DR Gramene; Q9FTT3; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004853; DUF250.
DR InterPro; IPR004696; Tpt_PEP_transl.
DR Pfam; PF03151; DUF250; 1.
DR TIGRFAMS; TIGR00817; tpt; 1.
SQ SEQUENCE 417 AA; 44643 MW; 32BAE1930715E38B CRC64;

Query Match 12.2%; Score 79.5; DB 2; Length 417;
Best Local Similarity 23.3%; Pred. No. 4.1;
Matches 28; Conservative 25; Mismatches 40; Indels 27; Gaps 5;

QY 8 FGKWWYFISAIENFGPRYLHGVPF-YFLILVR-----IISFLIGMEDVLLNCTLL 58
Db 120 FFMW-YFLNVFIENILNKKIYNFPYFVSVIHLVGWVYCLVSWTGLPKRAPINSTLL 178

QY 59 KRSSRRFRFGALVCSMDSCFRSRAVAVTY-----RFTLLNIPSPAVVMA 102
Db 179 KLLFPVALCHALGHVTSNVSFATVAVSFPAHTIKALEPFFNAAATQVLGQQVPLP-LWLUS 237

RESULT 3
Q9ARH5 PRELIMINARY; PRT; 417 AA.
AC Q9ARH5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Triose phosphate/phosphate translocator.
OS Oryza sativa (rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Erihartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang Q., Chen J., Wang X., Sun J., Sha W.;
RT "Molecular cloning and expression analysis of the rice triose
phosphate/phosphate translocator gene."
RL Plant Sci. 162:785-790(2002).
DR EMBL; AY028422; AAK27373.1; -
DR Gramene; Q9ARH5; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.

DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004853; DUF250.
DR InterPro; IPR004696; Tpt_PEP_transl.
DR Pfam; PF03151; DUF250; 1.
DR TIGRFAMS; TIGR00817; tpt; 1.
SQ SEQUENCE 417 AA; 44468 MW; 8E90D3DAAAD7853C CRC64;

Query Match 12.0%; Score 78; DB 2; Length 417;
Best Local Similarity 27.3%; Pred. No. 6;
Matches 24; Conservative 20; Mismatches 34; Indels 10; Gaps 3;

QY 8 FGKWWYFISAIENFGPRYLHGVPF-YFLILVR-----IISFLIGMEDVLLNCTLL 58
Db 120 FFMW-YFLNVFIENILNKKIYNFPYFVSVIHLVGWVYCLVSWTGLPKRAPINSTLL 178

QY 59 KRSSRRFRFGALVCSMDSCFRSRAVAVTY 86
Db 179 KLLFPVALCHALGHVTSNVSFATVAVSF 206

RESULT 4
Q40568 PRELIMINARY; PRT; 401 AA.
AC Q40568;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Phosphate translocator precursor.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]_TaxID=4097;
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=94166771; PubMed=8121415;
RA Knight J.S., Gray J.C.;
RT "Expression of genes encoding the tobacco chloroplast phosphate
translocator is not light-regulated and is repressed by sucrose.";
RL Mol. Gen. Genet. 242:586-594(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Gray J.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; X75088; CAAS2979.1; -
DR PIR; S42583; S42583.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004853; DUF250.
DR InterPro; IPR004696; Tpt_PEP_transl.
DR Pfam; PF03151; DUF250; 1.
DR TIGRFAMS; TIGR00817; tpt; 1.
KW Signal.
FT SIGNAL 1 73 Potential.
FT CHAIN 74 401 phosphate translocator.
SQ SEQUENCE 401 AA; 43705 MW; 36CC65B59A945035 CRC64;

Query Match 11.9%; Score 77.5; DB 2; Length 401;
Best Local Similarity 25.0%; Pred. No. 6.5;
Matches 30; Conservative 24; Mismatches 39; Indels 27; Gaps 5;

QY 8 FGKWWYFISAIENFGPRYLHGVPF-YFLILVR-----IISFLIGMEDVLLNCTLL 58
Db 103 FFMW-YFLNVFIENILNKKIYNFPYFVSVIHLVGWVYCLVSWTGLPKRAPIDSTQL 161

QY 59 KRSSRRFRFGALVCSMDSCFRSRAVAVTY-----RFTLLNIPSPAVVMA 102
Db 162 KLLTPVAFCHALGHVTSNVSFATVAVSFTHTIKALEPFFNAAATQVLGQQIPL-LWLUS 220

[illegible]

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RA Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Gigliotti E.A.,
RA Goeb-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.,
RA Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T.,
RA Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
RA de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
RA Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.,
RT "Comparative genomics of two Leptospira interrogans serovars reveals
RT novel insights into physiology and pathogenesis.";
RL J. Bacteriol. 186:2164-2172(2004).
DR EMBL; AE016824; AAS72189.1; -.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR001296; Glyco trans 1.
DR Pfam; PF00534; Glycos_transf_1; I.
KW Complete proteome.
SQ SEQUENCE 380 AA; 43772 MW; FB289EA9C63D6D6F CRC64;

Query Match 11.4%; Score 74.5; DB 2; Length 380;
Best Local Similarity 28.6%; Pred. No. 13;
Matches 28; Conservative 13; Mismatches 44; Indels 13; Gaps 5;

Qy 25 YLHGVPFFYLVRITS-----FLIGDMEDVL-LNCTLLKRSRFR---FWGALVCSM 74
||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 49 YLYSNKPIH-TVFYDILSNPNRSRFFMTGKPGIILNCTVPKRISKORLDFWGTQLLP 107
||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 75 DSCRFSRVAVTYRFTLLNIPSPAVVMARNTIDQOVLS 112
||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 108 LICGGALTAVNHDNLNFR--AAPXTMTTNSFWQHKILS 143

RESULT 12
Q8EXK4 PRELIMINARY; PRT; 380 AA.
AC Q8EXK4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mannosyltransferase A.
GN Name=ntfa; OrderedLocusNames=LB204;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AE011608; AAN51763.1; -.
DR GO; GO:0009058; P:biosynthesis; IEA.
KW Complete proteome.
SQ SEQUENCE 380 AA; 43772 MW; FB289EA9C63D6D6F CRC64;

Query Match 11.4%; Score 74.5; DB 2; Length 380;
Best Local Similarity 28.6%; Pred. No. 13;
Matches 28; Conservative 13; Mismatches 44; Indels 13; Gaps 5;

Qy 25 YLHGVPFFYLVRITS-----FLIGDMEDVL-LNCTLLKRSRFR---FWGALVCSM 74
||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 49 YLYSNKPIH-TVFYDILSNPNRSRFFMTGKPGIILNCTVPKRISKORLDFWGTQLLP 107
||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 75 DSCRFSRVAVTYRFTLLNIPSPAVVMARNTIDQOVLS 112
||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 108 LICGGALTAVNHDNLNFR--AAPXTMTTNSFWQHKILS 143

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RESULT 13
Q88W47 PRELIMINARY; PRT; 449 AA.
ID Q88W47;
AC Q88W47;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Integral membrane protein.
GN OrderedLocusNames=lp_1815;
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566; DOI=10.1073/pnas.0337704100;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
DR EMBL; AL935257; CAD64224.1; -.
KW Complete proteome.
SQ SEQUENCE 449 AA; 50073 MW; 59A911D45E3E474B CRC64;

Query Match 11.4%; Score 74.5; DB 2; Length 449;
Best Local Similarity 22.5%; Pred. No. 15;
Matches 32; Conservative 23; Mismatches 40; Indels 47; Gaps 7;

Qy 8 FGKW-VYFISAFNFG-----PRLYHG-----VFFVFLI 36
||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 277 FGKGMVLFVFAIYLLGPGTCRPLVLLGRHDLHRTTIARGLLVGHLLVATAQPLVVA 336
||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 37 LVRIISFLIGDMEDVLLNCTL-----LKRSSRFHWGALVCSMDSRFRVAV- 84
||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 337 GLLIISLYVG-FENPAINTSVYATEVNDPDLAIHKYRSTYGLGLLQCL--CFFGLLVIV 393
||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 85 -TVRFITLLNIPSPAVVMARNT 105
||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 394 SSFQQLNLLNFFNPASTALKNT 415

RESULT 14
Q7RIC2 PRELIMINARY; PRT; 462 AA.
ID Q7RIC2;
AC Q7RIC2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GUP 306 47338 45950.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB0100028; EAA41122.1; -.
SQ SEQUENCE 462 AA; 52140 MW; 278538F81B35F016 CRC64;

Query Match 11.4%; Score 74.5; DB 2; Length 462;
Best Local Similarity 24.2%; Pred. No. 16;
Matches 36; Conservative 20; Mismatches 50; Indels 43; Gaps 8;

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 90.3583 Seconds
(without alignments)
522.196 Million cells updates/sec

Title: US-10-092-934-2

Perfect score: 651

Sequence: 1 MMVWNRFGKVVVFISAFN.....RNTIDQQVLSRIKLEIKRCL 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Genesep16Dec04:*

1: Genesep1980s:*

2: Genesep1990s:*

3: Genesep2000s:*

4: Genesep2001s:*

5: Genesep2002s:*

6: Genesep2003as:*

7: Genesep2003bs:*

8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	651	100.0	122	2	AAR63237 Neural th
2	651	100.0	122	2	AAR95916 AD 3-4 hu
3	651	100.0	122	5	AAE29143 Neural th
4	651	100.0	122	6	ABR63241 122 amino
5	651	100.0	122	6	ABU02973 Human neu
6	651	100.0	122	6	ABP59924 Human 122
7	651	100.0	122	6	AAE33190 Neural th
8	651	100.0	122	6	ABJ19446 122-mer n
9	651	100.0	122	7	ADB37520 Neural th
10	651	100.0	122	7	ADL96022 Human neu
11	94	14.4	15	6	ABP59884 Human neu
12	94	14.4	15	7	ADL96030 Human neu
13	84	12.9	15	6	ABP59885 Human neu
14	84	12.9	15	7	ADL96031 Human neu
15	83	12.7	15	6	ABP59888 Human neu
16	83	12.7	15	7	ADL96034 Human neu
17	82	12.6	17	6	ABP59883 Human neu
18	82	12.6	17	7	ADB37533 Neural th
19	82	12.6	17	7	ADL96029 Human neu
20	80	12.3	15	6	ABP59890 Human neu
21	80	12.3	15	7	ADL96036 Human neu
22	78	12.0	15	6	ABP59887 Human neu
23	78	12.0	15	7	ADL96033 Human neu
24	77	11.8	15	6	ABP59889 Human neu
25	77	11.8	15	7	ADL96035 Human neu

26	76	11.7	320	6	ABP80429 N. gonorr
27	76	11.7	515	7	ABO65789 Klebsiell
28	74.5	11.4	239	3	AAG05704 Arabidops
29	74.5	11.4	320	3	AAG05703 Arabidops
30	74.5	11.4	321	3	AAG05702 Arabidops
31	73.5	11.3	118	5	AAM48171 Human dih
32	73.5	11.3	515	8	ADO28999 Mouse nov
33	73	11.2	15	6	ABP59886 Human neu
34	73	11.2	15	7	ADL96032 Human neu
35	72	11.1	345	7	ABM73876 DNA clone
36	72	11.1	347	7	ABM74181 DNA clone
37	72	11.1	1008	4	ABB70613 Drosophil
38	71.5	11.0	798	6	ABU37842 Protein e
39	71.5	11.0	805	3	AAV75603 Neisseria
40	71.5	11.0	805	3	AAV75601 Neisseria
41	71.5	11.0	805	3	AAV75602 Neisseria
42	71.5	11.0	805	6	ABP77700 N. gonorr
43	71.5	11.0	805	6	ABU37483 Protein e
44	68.5	10.5	178	2	AAV60130 Human end
45	68.5	10.5	1337	8	ADJ50050 Oil-assoc

ALIGNMENTS

RESULT 1

AAR63237
ID AAR63237 standard; protein; 122 AA.

XX AC AAR63237;

XX AC AAR63237;

DT 25-MAR-2003 (revised)

DT 06-JUL-1995 (first entry)

XX Neural thread protein AD3-4.

XX Neural thread protein AD3-4.

KW Neural thread protein AD3-4; Alzheimer's; neuroectodermal tumours;

KW malignant astrocytomas; glioblastomas.

XX Rattus rattus.

OS Rattus rattus.

FH Key Location/Qualifiers

FT Misc-difference 69..122

FT /note= "corresponding codons CTT TGG TCT GCT CGA TGG ATT

FT CTT GTC GAR TTT CTC GTG TGG CAG"

XX WO9423756-A1.

XX 27-OCT-1994.

XX 20-APR-1994; 94WO-US004321.

XX 20-APR-1993; 93US-00050559.

XX (GEHO) GEN HOSPITAL CORP.

XX De La Monte SM, Wands JR;

XX WPI; 1994-341497/42.

XX N-PSDB; AAG77875.

XX Detection of neural thread proteins - to detect sporadic and familial

XX Alzheimer's disease, neuroectodermal tumours, malignant astrocytomas and

XX glioblastomas (Eng).

XX Example 4; Fig 16f; 158pp; English.

XX AAQ77875 encodes AAR63237 the AD3-4 neural thread protein (NTP). These

XX sequences were used in the development of an antibody dependent method,

XX for the detection of NTPs. This new method could be used to diagnose

XX Alzheimer's disease (differentiating between sporadic and familial,

XX neuroectodermal tumours, malignant astrocytomas and glioblastomas.

XX (Updated on 25-MAR-2003 to correct PN field.)

```

XX SQ Sequence 122 AA;
Query Match 100.0%; Score 651; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.9e-73;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVCNRFKGVYFISAIENFGPRYLYHGVPFFYLILVRIISFLIGDMEDVLLNCTLLKR 60
    |||||
Db 1 MMVCNRFKGVYFISAIENFGPRYLYHGVPFFYLILVRIISFLIGDMEDVLLNCTLLKR 60
    |||||

QY 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVVMARNTIDQQVLSRIKLEIKR 120
    |||||
Db 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVVMARNTIDQQVLSRIKLEIKR 120
    |||||

QY 121 CL 122
    ||
Db 121 CL 122
    ||

RESULT 3
AAE29143
ID AAE29143 standard; protein; 122 AA.
XX AC AAE29143;
XX DT 27-JAN-2003 (first entry)
XX DE Neural thread protein (NTP) #1.
XX KW Neural thread protein; NTP; hyperplasia; hypertrophy; arteriosclerosis;
KW haemorrhoid; gene therapy; tumour; vascular disease; atherosclerosis;
KW inflammatory disease; nutritional deficiency disease; genetic disease;
KW autoimmune disease; metabolic disease; traumatic disease; intoxication;
KW infectious disease; congenital malformation; enzyme deficiency disease;
KW amyloid disease; fibrosis disease; storage disease; radiation disease;
KW poisoning; environmental disease; endocrine disease; protein therapy;
KW degenerative disease; mechanical disease.
XX OS Unidentified.
XX PN WO200274323-A2.
XX PD 26-SEP-2002.
XX PF 08-MAR-2002; 2002WO-IB001959.
XX PR 08-MAR-2001; 2001US-0273957P.
XX PA (AVER/) AVERBACK P.
XX PI Averbach P;
XX DR WPI; 2002-759864/82.
XX PT Treating a condition in a patient requiring removal or destruction of
PT cells, such as a benign or malignant tumor of a tissue or an inflammatory
PT disease, comprises administering a neural thread protein (NTP) or a NTP
PT gene to a mammal.
XX PS Claim 23; Fig 2; 70pp; English.
XX CC The invention relates to a method for treating a condition in a patient
CC requiring removal or destruction of cells. The method involves
CC administering to a mammal a neural thread protein (NTP), or administering
CC to a tumour or other target cell a NTP gene, where the expression of the
CC NTP gene is induced resulting in expression of the NTP protein. The
CC method and NTP are useful for treating a condition in a patient requiring
CC removal or destruction of cells, such as a benign or malignant tumour of
CC a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue,
CC preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,
CC bacterially, or parasitically altered tissue, or a malformation of a
CC tissue. Other conditions include a cosmetic modification to a tissue,
CC such as removal of unwanted facial hair, warts or unwanted fatty tissue,
CC a vascular disease, particularly atherosclerosis or arteriosclerosis,
CC haemorrhoids, or varicose veins, an inflammatory disease, autoimmune
CC disease, metabolic disease, hereditary/genetic disease, traumatic disease
CC or physical injury, nutritional deficiency disease, infectious disease,
CC congenital malformation, amyloid disease, fibrosis disease, storage

```

CC disease, enzyme deficiency disease, poisoning, intoxication, degenerative
CC disease, radiation disease, environmental disease, endocrine disease or
CC mechanical disease. The invention is useful in protein therapy and gene
CC therapy. The present sequence is NTP protein

XX SQ Sequence 122 AA;
Query Match 100.0%; Score 651; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.9e-73;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MMVCNRFQKVVYFISAFNFGPRYLHGVPFFFLILVRIISFLIGDMEDVLLNCTLLKR 60
Db 1 MMVCNRFQKVVYFISAFNFGPRYLHGVPFFFLILVRIISFLIGDMEDVLLNCTLLKR 60
Qy 61 SSRFRFGALVCSMDSCRSFSAVYTFITLLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120
Db 61 SSRFRFGALVCSMDSCRSFSAVYTFITLLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120
Qy 121 CL 122
Db 121 CL 122

RESULT 4

ABR63241
ID ABR63241 standard; protein; 122 AA.

XX AC ABR63241;

XX XX 28-AUG-2003 (first entry)

XX DE 122 amino acid neural thread protein.

XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour.

XX OS Unidentified.

XX WO2003008443-A2.

XX 30-JAN-2003.

XX 19-JUL-2002; 2002WO-CA001105.

XX 19-JUL-2001; 2001US-0306150P.

XX 19-JUL-2001; 2001US-0306161P.

XX 16-NOV-2001; 2001US-0331477P.

XX (NTMO-) NYMOX CORP.

XX Averbak PA;

XX WPI; 2003-247999/24.

XX Novel neural thread protein peptide, referred as cell death peptide,
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.

XX Disclosure; Fig 2; 77pp; English.

XX The present invention relates to a neural thread protein (NTP) peptide
CC referred to as cell death peptide. Thought to be cytostatic,
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC treating a condition in a patient requiring removal or destruction of
CC cells, for treating a condition such as benign or malignant tumor.
CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for
CC a pancreatic thread protein. The peptide is conjugated, linked or bound
CC to a molecule chosen from antibody or its fragment, antibody-like binding
CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side

CC effects of surgery. The present sequence is an NTP amino acid sequence
XX SQ Sequence 122 AA;

Query Match 100.0%; Score 651; DB 6; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.9e-73;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MMVCNRFQKVVYFISAFNFGPRYLHGVPFFFLILVRIISFLIGDMEDVLLNCTLLKR 60
Db 1 MMVCNRFQKVVYFISAFNFGPRYLHGVPFFFLILVRIISFLIGDMEDVLLNCTLLKR 60
Qy 61 SSRFRFGALVCSMDSCRSFSAVYTFITLLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120
Db 61 SSRFRFGALVCSMDSCRSFSAVYTFITLLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120
Qy 121 CL 122
Db 121 CL 122

RESULT 5

ABU02973
ID ABU02973 standard; protein; 122 AA.

XX AC ABU02973;

XX DT 20-JAN-2003 (first entry)

XX DE Human neural thread protein AD7C-NTP, protein fragment #1.

XX KW Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;
KW transplantation; grafting; chemotherapy; immunotherapy; vaccination;
KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;
KW radiation; tumour; hyperplasia; hypertrophy; overgrowth of tissue;
KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;
KW cosmetic modification; vascular disease; atherosclerosis;
KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;
KW autoimmune disease; metabolic disease; traumatic disease;
KW physical injury; nutritional deficiency disease; infectious disease;
KW amyloid disease; fibrosis disease; storage disease;
KW congenital malformation; enzyme deficiency disease; poisoning;
KW intoxication; environmental disease; radiation disease;
KW endocrine disease; degenerative disease; mechanical disease.

XX OS Homo sapiens.

XX WO200297030-A2.

XX PD 05-DEC-2002.

XX 24-MAY-2002; 2002WO-CA000759.

XX 25-MAY-2001; 2001US-0293156P.

XX (NYMO-) NYMOX CORP.

XX Averbak PA;

XX WPI; 2003-041406/03.

XX Novel peptides similar in amino acid sequence to neural thread proteins
PT (NTP), useful for treating unwanted cellular proliferations such as
PT malignant tumors and prostatic hyperplasia.

XX Disclosure; Fig 2; 78pp; English.

XX The invention describes an NTP-peptide (I) comprising at least one amino
CC acid sequence corresponding to part of the amino acid sequence of a
CC neural thread protein, AD7C-NTP. The invention provides a method of
CC treating a condition requiring removal or destruction of cells of a
CC mammal comprising administering to a mammal, a therapeutic amount of (I).
CC The treatment is administered to the mammal before, during or after

CC surgical excision, transplantation, grafting, chemotherapy,
CC immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,
CC laser therapy, phototherapy, gene therapy and/or radiation. The method is
CC useful for treatment of benign or malignant tumour; hyperplasia,
CC hypertrophy or overgrowth of tissue; virally, bacterially or
CC parasitically altered tissue; malformation of tissue selected from lung,
CC breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,
CC sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary
CC gland, blood, brain and its coverings, spinal cord, muscle, connective
CC tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary,
CC reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,
CC tonsils, mouth and lymph nodes and lymphoid system; tonsillary
CC hypertrophy; prostatic hyperplasia; cosmetic modification to a tissue;
CC vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;
CC varicose veins; inflammatory disease; autoimmune disease; metabolic
CC disease; hereditary/genetic disease; traumatic disease; physical injury;
CC nutritional deficiency disease; infectious disease; amyloid disease;
CC fibrosis disease; storage disease; congenital malformation; enzyme
CC deficiency disease; poisoning; intoxication; environmental disease;
CC radiation disease; endocrine disease; degenerative disease and mechanical
CC disease. This is the amino acid sequence of a human neural thread protein
CC AD7C-NTP protein fragment
XX
SQ Sequence 122 AA;

Query Match 100.0%; Score 651; DB 6; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.9e-73;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVCNRFCKWVYFISAIENFGPRYLHGVPFFLLVRIISFLIGDMEDVLLNCTLLKR 60
DB 1 MMVCNRFCKWVYFISAIENFGPRYLHGVPFFLLVRIISFLIGDMEDVLLNCTLLKR 60

QY 61 SSRFRFWGALVCSMDSCRSRVAVTYRFTLLNIPSPAVVMARNTIDQVLSRIKLEIKR 120
DB 61 SSRFRFWGALVCSMDSCRSRVAVTYRFTLLNIPSPAVVMARNTIDQVLSRIKLEIKR 120

QY 121 CL 122
DB 121 CL 122

RESULT 6
ABP5924
ID ABP5924 standard; protein; 122 AA.
XX
AC ABP5924;
XX
DT 08-SEP-2003 (first entry)
XX
DE Human 122 amino acid neural thread protein.
XX
KW Human; tumour; cancer; neural thread protein; NTP; cell removal;
KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;
KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN W02003044053-A2.
XX
PD 30-MAY-2003.
XX
PF 18-NOV-2002; 2002WO-CA001757.
XX
PR 16-NOV-2001; 2001US-0331477P.
XX
PA (NYMO-) NYMOX CORP.
XX
PI Averback P, Gemmell J;
XX WPI; 2003-457592/43.
XX

PT New neural thread protein (NTP), useful for preparing a composition for
PT treating or preventing a condition in a mammal requiring removal or
PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or
PT inflammatory disease.
XX
PS Disclosure; Fig 1; 98pp; English.
XX
CC The present invention relates to peptides derived from the human neural
CC thread protein (NTP). The peptides are useful for preparing a composition
CC for treating or preventing a condition in a mammal requiring removal or
CC destruction of cells, comprising tonsillary hypertrophy, prostatic
CC hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a
CC breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,
CC varicose veins, atherosclerosis, inflammatory, metabolic, infectious,
CC fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,
CC occlusion or blockage of an artery or of a stent placed or implanted in
CC an artery. The present sequence is an NTP protein used to produce
CC peptides of the invention
XX
SQ Sequence 122 AA;

Query Match 100.0%; Score 651; DB 6; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.9e-73;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVCNRFCKWVYFISAIENFGPRYLHGVPFFLLVRIISFLIGDMEDVLLNCTLLKR 60
DB 1 MMVCNRFCKWVYFISAIENFGPRYLHGVPFFLLVRIISFLIGDMEDVLLNCTLLKR 60

QY 61 SSRFRFWGALVCSMDSCRSRVAVTYRFTLLNIPSPAVVMARNTIDQVLSRIKLEIKR 120
DB 61 SSRFRFWGALVCSMDSCRSRVAVTYRFTLLNIPSPAVVMARNTIDQVLSRIKLEIKR 120

QY 121 CL 122
DB 121 CL 122

RESULT 7
AAE33190
ID AAE33190 standard; protein; 122 AA.
XX
AC AAE33190;
XX
DT 16-APR-2003 (first entry)
XX
DE Neural thread protein (NTP) #1.
XX
KW Cell death; tissue necrosis; neural thread protein; NTP; amyloidosis;
KW stroke; brain tumour; Pick's disease; Parkinson's disease; glaucoma;
KW Alzheimer's disease; gene therapy.
XX
OS Unidentified.
XX
PN W0200289841-A2.
XX
PD 14-NOV-2002.
XX
PF 06-MAY-2002; 2002WO-CA000681.
XX
PR 04-MAY-2001; 2001US-0288463P.
XX
PA (NYMO-) NYMOX CORP.
XX
PI Averback PA;
XX
DR WPI; 2003-120506/11.
XX
PT Preventing, controlling, modulating, ameliorating and/or treating cell
PT death or tissue necrosis using antibodies to neural thread proteins,
PT useful in disorders such as stroke, brain tumor, glaucoma and Alzheimer's
PT disease.
XX

PS Disclosure; Fig 5; 60pp; English.

XX The invention relates to a method of preventing, and/or inhibiting cell

CC death and/or tissue necrosis in live tissue containing neural thread

CC proteins (NTP). The method involves contacting the live tissue with at

CC least one antibody, fragment or derivative that recognises NTP, where the

CC antibody, fragment or derivative is present to prevent, control,

CC ameliorate and/or inhibit cell death and/or tissue necrosis caused by the

CC presence of NTP. Methods and compositions of the invention are useful for

CC preventing, modulating, controlling and/or treating disorders associated

CC with cell death and/or tissue necrosis such as stroke, brain tumour,

CC Pick's disease, Parkinson's disease, amyloidosis, glaucoma and

CC Alzheimer's disease. The invention is useful in gene therapy. The present

CC sequence is NTP protein

XX

SQ Sequence 122 AA;

Query Match 100.0%; Score 651; DB 6; Length 122;

Best Local Similarity 100.0%; Pred. No. 1.9e-73;

Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVCNRFKGVYFISAIENFGPRYLHGVPFFYLILVRIISFLIGMEDVLLNCTLLKR 60

Db 1 MMVCNRFKGVYFISAIENFGPRYLHGVPFFYLILVRIISFLIGMEDVLLNCTLLKR 60

Qy 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120

Db 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120

Qy 121 CL 122

Db 121 CL 122

RESULT 8

ABJ19446

ID ABJ19446 standard; protein; 122 AA.

XX

AC ABJ19446;

XX

DT 27-MAR-2003 (first entry)

XX

DE 122-mer neural thread protein.

XX

KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;

KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.

XX

OS Unidentified.

XX

PN WO200292115-A2.

XX

PD 21-NOV-2002.

XX

PF 16-MAY-2002; 2002WO-CA000712.

XX

PR 16-MAY-2001; 2001US-0290971P.

XX

PA (NYMO-) NYMOX CORP.

XX

PI Averbach PA;

XX

PS WPI; 2003-129234/12.

XX

PT Preventing and/or inhibiting cell death and/or tissue necrosis in a

PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's

PT disease, by contacting the live tissue with at least one segment of

PT neural thread proteins (NTP).

XX

PS Disclosure; Fig 2; 60pp; English.

XX

XX The invention relates to a novel method for preventing and/or inhibiting

CC cell death and/or tissue necrosis in a tissue comprising contacting the

CC live tissue with at least one segment of neural thread proteins (NTP).

CC

CC The methods are composition are useful for treating a neurodegenerative

CC disorder, such as Alzheimer's disease. This sequence represents an NTP

CC protein of the invention

XX

SQ Sequence 122 AA;

Query Match 100.0%; Score 651; DB 6; Length 122;

Best Local Similarity 100.0%; Pred. No. 1.9e-73;

Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVCNRFKGVYFISAIENFGPRYLHGVPFFYLILVRIISFLIGMEDVLLNCTLLKR 60

Db 1 MMVCNRFKGVYFISAIENFGPRYLHGVPFFYLILVRIISFLIGMEDVLLNCTLLKR 60

Qy 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120

Db 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120

Qy 121 CL 122

Db 121 CL 122

RESULT 9

ADB37520

ID ADB37520 standard; protein; 122 AA.

XX

AC ADB37520;

XX

DT 04-DEC-2003 (first entry)

XX

DE Neural thread protein #1.

XX

KW Cytostatic; Antitumour; Antipsoriatic; Dermatological;

KW Antiatherosclerotic; Antiarteriosclerotic; Vasotropic; Antiinflammatory;

KW Immunosuppressive; Tranquillizer; Antiemetic; Virucide; AD7c-NTP;

KW neural thread protein; neuritic sprouting.

XX

OS Unidentified.

XX

PN WO2003008444-A2.

XX

PD 30-JAN-2003.

XX

PF 19-JUL-2002; 2002WO-CA001106.

XX

PR 19-JUL-2001; 2001US-0306150P.

XX

PR 19-JUL-2001; 2001US-0306161P.

XX

PR 16-NOV-2001; 2001US-0331477P.

XX

PA (NYMO-) NYMOX CORP.

XX

PI Averbach PA, Gemmell J;

XX

PS WPI; 2003-248000/24.

XX

PT Novel Related peptide or AD7c-neural thread peptide, useful for treating

PT unwanted cellular proliferations, glandular hyperplasia, unwanted facial

PT hair, warts and unwanted fatty tissue.

XX

PS Disclosure; Fig 2; 109pp; English.

XX

XX The present invention relates to AD7c-neural thread protein (NTP) and

CC related proteins and peptides (I; ADB37528-ADB37641). The sequences are

CC useful for treating a condition in a patient requiring removal or

CC destruction of cells. The condition can be selected from benign or

CC malignant tumour of a tissue, hyperplasia, hypertrophy or overgrowth of a

CC tissue, virally, bacterially or parasitically altered tissue, or

CC malformation of a tissue, where the tissue is selected from lung, breast,

CC stomach, pancreas, prostate, bladder, bone, ovary, kidney, sinus,

CC colon, intestine, stomach, rectum, oesophagus, heart, spleen, salivary

CC gland, blood, brain and its coverings, spinal cord and its coverings,

CC muscle, connective tissue, adrenal, parathyroid, thyroid, uterus, testis,

CC

CC pituitary, reproductive organs, liver, gall bladder, eye, ear, nose,
 CC throat, tonsils, mouth, lymph nodes and lymphoid tissue. The condition is
 CC preferably tonsillary hypertrophy, prostatic hyperplasia, psoriasis,
 CC eczema, dermatosis, cosmetic modification to a tissue (skin, eye, ear,
 CC nose, throat, mouth, muscle, connective, hair or breast tissue), vascular
 CC disease (atherosclerosis or arteriosclerosis), haemorrhoids, varicose
 CC veins, inflammatory disease, autoimmune disease, metabolic disease,
 CC hereditary/genetic disease, traumatic disease or physical injury,
 CC nutritional deficiency disease, infectious disease, amyloid disease,
 CC fibrosis disease, storage disease, congenital malformation, enzyme
 CC deficiency disease, poisoning, intoxication, environmental disease,
 CC radiation disease, endocrine disease, degenerative disease and mechanical
 CC disease. The peptides are useful for treating unwanted cellular
 CC proliferations, glandular (e.g. prostate) hyperplasia, unwanted facial
 CC hair, warts and unwanted fatty tissue, or for preparing antibodies that
 CC recognize and/or bind to Related proteins, Related peptides or NTP
 CC peptides. The present sequence was used to illustrate the invention.

XX Sequence 122 AA;

Query Match 100.0%; Score 651; DB 7; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.9e-73;
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVCWNRFGKVVYFISAIENFGPRYLHGVPFFLLILVRIISFLIGDMEDVLLNCTLLKR 60
 |||||
 DB 1 MMVCWNRFGKVVYFISAIENFGPRYLHGVPFFLLILVRIISFLIGDMEDVLLNCTLLKR 60
 |||||
 QY 61 SSRFRFWGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAENTIDQVLSRIKLEIKR 120
 |||||
 DB 61 SSRFRFWGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAENTIDQVLSRIKLEIKR 120
 |||||
 QY 121 CL 122
 ||
 DB 121 CL 122

RESULT 10
 ADL96022

ID ADL96022 standard; protein; 122 AA.

XX ADL96022;

DT 20-MAY-2004 (first entry)

XX Human neural thread protein, NTP122.

XX Human; neural thread protein; NTP122; NTP112; NTP106; NTP98; NTP75;
 KW NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;
 KW eczema; haemorrhoid; atherosclerosis; inflammatory disease;
 KW autoimmune disease; metabolic disease; hereditary disease;
 KW genetic disease; traumatic disease; physical injury;
 KW nutritional deficiency disease; infectious disease; amyloid disease;
 KW Alzheimer's disease; storage disease; congenital malformation;
 KW enzyme deficiency disease; poisoning; intoxication;
 KW environmental disease; radiation disease; endocrine disease;
 KW degenerative disease; mechanical disease.

XX Homo sapiens.

XX US2003166569-A1.

XX 04-SEP-2003.

XX 15-NOV-2002; 2002US-00294891.

XX 16-NOV-2001; 2001US-0331477P.

XX (AVER/) AVERBACK P.
 XX (GEMM/) GEMMELL J.

XX Averbach P, Gemmell J;

DR WPI; 2003-898099/82.
 XX New neural thread protein or its variants, useful for treating tumors and
 PT other conditions requiring the removal or destruction of cells (e.g.
 PT prostatic hyperplasia, psoriasis, eczema, hemorrhoids or
 PT atherosclerosis).

XX Disclosure; SEQ ID NO 1; 32pp; English.

XX The invention relates to a peptide, or its homologue, derivative,
 CC fragment, variant or mimetic, comprising at least one neural thread
 CC protein (NTP) peptide appearing as ADL96029-ADL96069, derived from
 CC NTP122, 112, 106, 98.75, 68 or 61. Also included are a nucleic acid
 CC encoding an amino acid sequence corresponding to the above peptide, a
 CC composition comprising one or more peptides or nucleic acids cited above
 CC and a carrier, a method of treating a condition in a mammal requiring
 CC removal or destruction of cells (comprising administering to the mammal
 CC an amount of the peptide cited above) and a method of preventing or
 CC inhibiting the stenosis, occlusion or blockage of a stent, comprising
 CC coating the stent with an amount of the above peptide. The peptide
 CC further comprises an amino acid in a reverse-D order based on the above
 CC amino acid sequences. The composition and methods are useful in treating
 CC tumours and other conditions requiring the removal or destruction of
 CC cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or
 CC atherosclerosis). These may also be used in treating inflammatory
 CC diseases, autoimmune diseases, metabolic diseases, hereditary/genetic
 CC diseases, traumatic diseases or physical injuries, nutritional deficiency
 CC diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,
 CC storage diseases, congenital malformation, enzyme deficiency diseases,
 CC poisoning, intoxication, environmental diseases, radiation diseases,
 CC endocrine diseases, degenerative diseases or mechanical diseases. The
 CC present sequence is a human NTP protein from which the peptides of the
 CC invention are derived.

XX Sequence 122 AA;

Query Match 100.0%; Score 651; DB 7; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.9e-73;
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVCWNRFGKVVYFISAIENFGPRYLHGVPFFLLILVRIISFLIGDMEDVLLNCTLLKR 60
 |||||

DB 1 MMVCWNRFGKVVYFISAIENFGPRYLHGVPFFLLILVRIISFLIGDMEDVLLNCTLLKR 60
 |||||

QY 61 SSRFRFWGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAENTIDQVLSRIKLEIKR 120
 |||||

DB 61 SSRFRFWGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAENTIDQVLSRIKLEIKR 120
 |||||

QY 121 CL 122

DB 121 CL 122

RESULT 11
 ABP59884

ID ABP59884 standard; peptide; 15 AA.

XX ABP59884;

XX 28-AUG-2003 (first entry)

XX Human neural thread protein NTP(122) peptide #2.

XX Human; tumour; cancer; neural thread protein; NTP; cell removal;
 KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;
 KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;
 KW gene therapy.

XX Homo sapiens.

XX WO2003044053-A2.

XX 30-MAY-2003.

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XX 18-NOV-2002; 2002WO-CA001757.
XX
XX 16-NOV-2001; 2001US-0331477P.
XX
XX (NYMO-) NYMOX CORP.
XX
XX Averbach P, Gemmell J;
XX
XX WPI; 2003-457592/43.
XX
XX New neural thread protein (NTP), useful for preparing a composition for
XX treating or preventing a condition in a mammal requiring removal or
XX destruction of cells, e.g. psoriasis, eczema, atherosclerosis or
XX inflammatory disease.
XX
XX Claim 1; Page 31; 98pp; English.
XX
XX The present invention relates to peptides derived from the human neural
XX thread protein (NTP). The peptides are useful for preparing a composition
XX for treating or preventing a condition in a mammal requiring removal or
XX destruction of cells, comprising tonsillary hypertrophy, prostatic
XX hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a
XX breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,
XX varicose veins, atherosclerosis, inflammatory, metabolic, infectious,
XX fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,
XX occlusion or blockage of an artery or of a stent placed or implanted in
XX an artery. The present sequence is a peptide of the invention
XX
XX Sequence 15 AA;
XX
XX Query Match 14.4%; Score 94; DB 6; Length 15;
XX Best Local Similarity 100.0%; Pred. NO. 0.00016;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 MMVCWNRFGKWVYFI 15
XX | | | | | | | | | |
XX Db 1 MMVCWNRFGKWVYFI 15
XX
XX RESULT 12
XX ID ADL96030 standard; peptide; 15 AA.
XX
XX AC ADL96030;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human neural thread protein, NTP122, peptide #2.
XX
XX Human; neural thread protein; NTP122; NTP106; NTP98; NTP75;
XX NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;
XX eczema; haemorrhoid; atherosclerosis; inflammatory disease;
XX autoimmune disease; metabolic disease; hereditary disease;
XX genetic disease; traumatic disease; physical injury;
XX nutritional deficiency disease; infectious disease; amyloid disease;
XX Alzheimer's disease; storage disease; congenital malformation;
XX enzyme deficiency disease; poisoning; intoxication;
XX environmental disease; radiation disease; endocrine disease;
XX degenerative disease; mechanical disease.
XX
XX Homo sapiens.
XX
XX OS
XX US2003166569-A1.
XX
XX 04-SEP-2003.
XX
XX 15-NOV-2002; 2002US-00294891.
XX
XX 16-NOV-2001; 2001US-0331477P.
XX
XX (AVER/) AVERBACK P.
XX (GEMM/) GEMMELL J.
XX
XX Averbach P, Gemmell J;
XX
XX WPI; 2003-898099/82.
XX
XX New neural thread protein or its variants, useful for treating tumors and
XX other conditions requiring the removal or destruction of cells (e.g.
XX prostatic hyperplasia, psoriasis, eczema, haemorrhoids or
XX atherosclerosis).
XX
XX Claim 1; SEQ ID NO 9; 32pp; English.
XX
XX The invention relates to a peptide, or its homologue, derivative,
XX fragment, variant or mimetic, comprising at least one neural thread
XX protein (NTP) peptide, appearing as ADL96030-ADL96069, derived from
XX NTP122, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid
XX encoding an amino acid sequence corresponding to the above peptide, a
XX composition comprising one or more peptides or nucleic acids cited above
XX and a carrier, a method of treating a condition in a mammal requiring
XX removal or destruction of cells (comprising administering to the mammal
XX an amount of the peptide cited above) and a method of preventing or
XX inhibiting the stenosis, occlusion or blockage of a stent, comprising
XX coating the stent with an amount of the above peptide. The peptide
XX further comprises an amino acid in a reverse-D order based on the above
XX amino acid sequences. The composition and methods are useful in treating
XX tumours and other conditions requiring the removal or destruction of
XX cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or
XX atherosclerosis). These may also be used in treating inflammatory
XX diseases, autoimmune diseases, metabolic diseases, hereditary/genetic
XX diseases, traumatic diseases or physical injuries, nutritional deficiency
XX diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,
XX storage diseases, congenital malformation, enzyme deficiency diseases,
XX poisoning, intoxication, environmental diseases, radiation diseases,
XX endocrine diseases, degenerative diseases or mechanical diseases. The
XX present sequence is a NTP peptide of the invention.
XX
XX Sequence 15 AA;
XX
XX Query Match 14.4%; Score 94; DB 7; Length 15;
XX Best Local Similarity 100.0%; Pred. NO. 0.00016;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 MMVCWNRFGKWVYFI 15
XX | | | | | | | | | |
XX Db 1 MMVCWNRFGKWVYFI 15
XX
XX RESULT 13
XX ABP59885
XX ID ABP59885 standard; peptide; 15 AA.
XX
XX AC ABP59885;
XX
XX 28-AUG-2003 (first entry)
XX
XX Human neural thread protein NTP(122) peptide #3.
XX
XX Human; tumour; cancer; neural thread protein; NTP; cell removal;
XX cell destruction; antipsoriatic; antimicrobial; immunosuppressive;
XX antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;
XX gene therapy.
XX
XX Homo sapiens.
XX
XX OS
XX WO2003044053-A2.
XX
XX 30-MAY-2003.
XX
XX 18-NOV-2002; 2002WO-CA001757.
XX
XX 16-NOV-2001; 2001US-0331477P.
XX
XX (NYMO-) NYMOX CORP.
XX

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XX Averback P, Gemmell J;
 XX WPI; 2003-457592/43.
 XX
 XX New neural thread protein (NTP), useful for preparing a composition for
 XX treating or preventing a condition in a mammal requiring removal or
 XX destruction of cells, e.g. psoriasis, eczema, atherosclerosis or
 XX inflammatory disease.
 XX
 XX Claim 1; Page 31; 98pp; English.
 XX
 XX The present invention relates to peptides derived from the human neural
 XX thread protein (NTP). The peptides are useful for preparing a composition
 XX for treating or preventing a condition in a mammal requiring removal or
 XX destruction of cells, comprising tonsillary hypertrophy, prostatic
 XX hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a
 XX breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,
 XX varicose veins, atherosclerosis, inflammatory, metabolic, infectious,
 XX fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,
 XX occlusion or blockage of an artery or of a stent placed or implanted in
 XX an artery. The present sequence is a peptide of the invention
 XX
 XX Sequence 15 AA;
 XX
 XX Query Match 12.9%; Score 84; DB 6; Length 15;
 XX Best Local Similarity 100.0%; Pred. No. 0.0029;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 16 SAIFNFGPRYLXGV 30
 XX | | | | | | | | | | | | | | | |
 XX Db 1 SAIFNFGPRYLXGV 15
 XX
 XX RESULT 14
 XX ADL96031
 XX ID ADL96031 standard; peptide; 15 AA.
 XX AC
 XX ADL96031;
 XX
 XX DT 20-MAY-2004 (first entry)
 XX
 XX DE Human neural thread protein, NTP122, peptide #3.
 XX
 XX Human; neural thread protein; NTP122; NTP106; NTP98; NTP75;
 XX NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;
 XX eczema; haemorrhoid; atherosclerosis; inflammatory disease;
 XX autoimmune disease; metabolic disease; hereditary disease;
 XX genetic disease; traumatic disease; physical injury;
 XX nutritional deficiency disease; infectious disease; amyloid disease;
 XX Alzheimer's disease; storage disease; congenital malformation;
 XX enzyme deficiency disease; poisoning; intoxication;
 XX environmental disease; radiation disease; endocrine disease;
 XX degenerative disease; mechanical disease.
 XX
 XX OS Homo sapiens.
 XX
 XX US2003166569-A1.
 XX
 XX PD 04-SEP-2003.
 XX
 XX PF 15-NOV-2002; 2002US-00294891.
 XX
 XX PR 16-NOV-2001; 2001US-0331477P.
 XX
 XX (AVER/) AVERBACK P.
 XX (GEMM/) GEMMELL J.
 XX
 XX Averback P, Gemmell J;
 XX WPI; 2003-898099/82.
 XX
 XX New neural thread protein or its variants, useful for treating tumors and

PT other conditions requiring the removal or destruction of cells (e.g.
 PT prostatic hyperplasia, psoriasis, eczema, hemorrhoids or
 PT atherosclerosis).
 XX
 XX Claim 1; SEQ ID NO 10; 32pp; English.
 XX
 XX The invention relates to a peptide, or its homologue, derivative,
 XX fragment, variant or mimetic, comprising at least one neural thread
 XX protein (NTP) peptide appearing as ADL96029-ADL96069, derived from
 XX NTP122, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid
 XX encoding an amino acid sequence corresponding to the above peptide, a
 XX composition comprising one or more peptides or nucleic acids cited above
 XX and a carrier, a method of treating a condition in a mammal requiring
 XX removal or destruction of cells (comprising administering to the mammal
 XX an amount of the peptide cited above) and a method of preventing or
 XX inhibiting the stenosis, occlusion or blockage of a stent, comprising
 XX coating the stent with an amount of the above peptide. The peptide
 XX further comprises an amino acid in a reverse-D order based on the above
 XX amino acid sequences. The composition and methods are useful in treating
 XX tumours and other conditions requiring the removal or destruction of
 XX cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or
 XX atherosclerosis). These may also be used in treating inflammatory
 XX diseases, autoimmune diseases, metabolic diseases, hereditary/genetic
 XX diseases, traumatic diseases or physical injuries, nutritional deficiency
 XX storage diseases, congenital malformation, enzyme deficiency diseases,
 XX poisoning, intoxication, environmental diseases, radiation diseases,
 XX endocrine diseases, degenerative diseases or mechanical diseases. The
 XX present sequence is a NTP peptide of the invention.
 XX
 XX Sequence 15 AA;
 XX
 XX Query Match 12.9%; Score 84; DB 7; Length 15;
 XX Best Local Similarity 100.0%; Pred. No. 0.0029;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 16 SAIFNFGPRYLXGV 30
 XX | | | | | | | | | | | | | | | |
 XX Db 1 SAIFNFGPRYLXGV 15
 XX
 XX RESULT 15
 XX ABP59888
 XX ID ABP59888 standard; peptide; 15 AA.
 XX AC
 XX ABP59888;
 XX
 XX DT 28-AUG-2003 (first entry)
 XX
 XX DE Human neural thread protein NTP(122) peptide #6.
 XX
 XX Human; tumour; cancer; neural thread protein; NTP; cell removal;
 XX cell destruction; antipsoriatic; antimicrobial; immunosuppressive;
 XX antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;
 XX gene therapy.
 XX
 XX OS Homo sapiens.
 XX
 XX WO2003044053-A2.
 XX
 XX PD 30-MAY-2003.
 XX
 XX PF 18-NOV-2002; 2002WO-CA001757.
 XX
 XX PR 16-NOV-2001; 2001US-0331477P.
 XX
 XX (NYMO-) NYMOX CORP.
 XX
 XX Averback P, Gemmell J;
 XX WPI; 2003-457592/43.
 XX
 XX New neural thread protein (NTP), useful for preparing a composition for

PT treating or preventing a condition in a mammal requiring removal or
PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or
PT inflammatory disease.
XX
PS Claim 1; Page 32; 98pp; English.
XX
CC The present invention relates to peptides derived from the human neural
CC thread protein (NTP). The peptides are useful for preparing a composition
CC for treating or preventing a condition in a mammal requiring removal or
CC destruction of cells, comprising tonsillary hypertrophy, prostatic
CC hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a
CC breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,
CC varicose veins, atherosclerosis, inflammatory, metabolic, infectious,
CC fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,
CC occlusion or blockage of an artery or of a stent placed or implanted in
CC an artery. The present sequence is a peptide of the invention
XX
SQ Sequence 15 AA;

Query Match 12.7%; Score 83; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 61 SSRFRFWGALVCSMD 75
Db 1 SSRFRFWGALVCSMD 15

Search completed: October 11, 2005, 07:10:58
Job time : 94.3583 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:16 ; Search time 204.529 Seconds
(without alignments)
248.149 Million cell updates/sec

Title: US-10-092-934-2

Perfect score: 651

Sequence: 1 MMVCNRFKGVYFISAI FN.....RNTIDQQVLSRIKLEIKRCL 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	651	100.0	122	14	US-10-138-516-1
2	651	100.0	122	14	US-10-146-130-3
3	651	100.0	122	14	US-10-092-934-2
4	651	100.0	122	14	US-10-153-334-2
5	651	100.0	122	14	US-10-198-069-2
6	651	100.0	122	14	US-10-198-070-2
7	651	100.0	122	14	US-10-294-891-1
8	651	100.0	122	17	US-10-920-313-1
9	94	14.4	15	14	US-10-294-891-9
10	94	14.4	15	17	US-10-920-313-9
11	84	12.9	15	14	US-10-294-891-10

12	84	12.9	15	17	US-10-920-313-10	Sequence 10, Appl
13	83	12.7	15	14	US-10-294-891-13	Sequence 13, Appl
14	83	12.7	15	17	US-10-920-313-13	Sequence 13, Appl
15	82	12.6	17	14	US-10-198-070-15	Sequence 15, Appl
16	82	12.6	17	14	US-10-294-891-8	Sequence 8, Appl
17	82	12.6	17	17	US-10-920-313-8	Sequence 8, Appl
18	80	12.3	15	14	US-10-294-891-15	Sequence 15, Appl
19	80	12.3	15	17	US-10-920-313-15	Sequence 15, Appl
20	78	12.0	15	14	US-10-294-891-12	Sequence 12, Appl
21	78	12.0	15	17	US-10-920-313-12	Sequence 12, Appl
22	77	11.8	15	14	US-10-294-891-14	Sequence 14, Appl
23	77	11.8	15	17	US-10-920-313-14	Sequence 14, Appl
24	75	11.5	402	16	US-10-739-930-10886	Sequence 10886, A
25	73	11.2	15	14	US-10-294-891-11	Sequence 11, Appl
26	73	11.2	15	17	US-10-920-313-11	Sequence 11, Appl
27	72	11.1	1008	20	US-11-097-143-38631	Sequence 38631, A
28	71.5	11.0	124	15	US-10-424-599-153047	Sequence 153047, A
29	71.5	11.0	798	15	US-10-282-122A-65766	Sequence 65766, A
30	71.5	11.0	805	15	US-10-282-122A-65407	Sequence 65407, A
31	71	10.9	204	15	US-10-425-114-37820	Sequence 37820, A
32	70	10.8	405	16	US-10-425-115-300362	Sequence 300362, A
33	70	10.8	410	16	US-10-425-115-291572	Sequence 291572, A
34	70	10.8	416	15	US-10-425-114-68863	Sequence 68863, A
35	69.5	10.7	311	15	US-10-424-599-191606	Sequence 191606, A
36	69	10.6	229	15	US-10-424-599-248193	Sequence 248193, A
37	68.5	10.5	1337	15	US-10-389-566-2054	Sequence 2054, Ap
38	68	10.4	104	17	US-10-732-923-12543	Sequence 12543, A
39	68	10.4	233	9	US-09-886-319A-11	Sequence 11, Appl
40	68	10.4	233	14	US-10-376-564-11	Sequence 11, Appl
41	68	10.4	929	15	US-10-436-323-3	Sequence 3, Appl
42	67.5	10.4	414	14	US-10-083-357-1274	Sequence 1274, Ap
43	67.5	10.4	645	16	US-10-437-963-182845	Sequence 182845, A
44	67	10.3	66	16	US-10-425-115-185032	Sequence 185032, A
45	67	10.3	340	16	US-10-437-963-129129	Sequence 129129, A

ALIGNMENTS

RESULT 1

US-10-138-516-1

; Sequence 1, Application US/10138516

; Publication No. US20030003445A1

; GENERAL INFORMATION:

; APPLICANT: AVERBACK, PAUL

; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING ANTIBODIES TO NEURAL THREAD PROTEINS

; FILE REFERENCE: 59003.000004

; CURRENT APPLICATION NUMBER: US/10/138,516

; CURRENT FILING DATE: 2002-07-23

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 122

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-138-516-1

Query Match 100.0%; Score 651; DB 14; Length 122;
Best Local Similarity 100.0%; Pred. No. 9.6e-70;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MMVCNRFKGVYFISAI FNPGPRYLHGVPFYFLILVRIISFLIGDMEDVLLNCTLLKR	60
Qy	61	SSRFRFGALVCSMDSCRFSSRVAVTYRITLNIPTSPAVMWRNTIDQQVLSRIKLEIKR	120
Db	61	SSRFRFGALVCSMDSCRFSSRVAVTYRITLNIPTSPAVMWRNTIDQQVLSRIKLEIKR	120
Qy	121	CL 122	
Db	121	CL 122	

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RESULT 2
US-10-146-130-3
; Sequence 3, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-3

Query Match      100.0%; Score 651; DB 14; Length 122;
Best Local Similarity 100.0%; Pred. No. 9.6e-70;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MMVCNRFCKWVYFISAIENFGPRYLHGVPFFLLVRIISFLIGDMEDVLLNCTLLKR 60
Db      1  MMVCNRFCKWVYFISAIENFGPRYLHGVPFFLLVRIISFLIGDMEDVLLNCTLLKR 60

Qy      61  SSRFRFGALVCSMDSCRSRVAVTYRFTITLLNIPSPAVMMARNTIDQQVLSRIKLEIKR 120
Db      61  SSRFRFGALVCSMDSCRSRVAVTYRFTITLLNIPSPAVMMARNTIDQQVLSRIKLEIKR 120

Qy      121  CL 122
Db      121  CL 122

RESULT 3
US-10-092-934-2
; Sequence 2, Application US/10092934
; Publication No. US20030054990A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHODS OF USING NEURAL THREAD PROTEINS TO TREAT TUMORS
; TITLE OF INVENTION: AND CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018792-0199
; CURRENT APPLICATION NUMBER: US/10/092,934
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/273,957
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Neural thread
US-10-092-934-2

Query Match      100.0%; Score 651; DB 14; Length 122;
Best Local Similarity 100.0%; Pred. No. 9.6e-70;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MMVCNRFCKWVYFISAIENFGPRYLHGVPFFLLVRIISFLIGDMEDVLLNCTLLKR 60
Db      1  MMVCNRFCKWVYFISAIENFGPRYLHGVPFFLLVRIISFLIGDMEDVLLNCTLLKR 60

Qy      61  SSRFRFGALVCSMDSCRSRVAVTYRFTITLLNIPSPAVMMARNTIDQQVLSRIKLEIKR 120
Db      61  SSRFRFGALVCSMDSCRSRVAVTYRFTITLLNIPSPAVMMARNTIDQQVLSRIKLEIKR 120

Qy      121  CL 122
Db      121  CL 122

RESULT 4
US-10-153-334-2
; Sequence 2, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003-000006
; CURRENT APPLICATION NUMBER: US/10/153,334
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,156
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-334-2

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Best Local Similarity 100.0%; Pred. No. 9.6e-70;
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Qy      1  MMVCNRFCKWVYFISAIENFGPRYLHGVPFFLLVRIISFLIGDMEDVLLNCTLLKR 60
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Qy      61  SSRFRFGALVCSMDSCRSRVAVTYRFTITLLNIPSPAVMMARNTIDQQVLSRIKLEIKR 120
Db      61  SSRFRFGALVCSMDSCRSRVAVTYRFTITLLNIPSPAVMMARNTIDQQVLSRIKLEIKR 120

Qy      121  CL 122
Db      121  CL 122

RESULT 5
US-10-198-069-2
; Sequence 2, Application US/10198069
; Publication No. US20030096756A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000009
; CURRENT APPLICATION NUMBER: US/10/198,069
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown NTP
; OTHER INFORMATION: peptide

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US-10-198-069-2

Query Match 100.0%; Score 651; DB 14; Length 122;
Best Local Similarity 100.0%; Pred. No. 9.6e-70;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MMVCNRFKGVVYFISAIENFGPRYLHGVPFFYLILVRIISFLIGDMEDVLLNCTLLKR 60

Qy 61 SSRFRFGALVCSMDSCRSRVAVTYRFTILLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120
Db 61 SSRFRFGALVCSMDSCRSRVAVTYRFTILLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120

Qy 121 CL 122
Db 121 CL 122

RESULT 6

US-10-198-070-2
; Sequence 2, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR FILING DATE: 2002-07-19
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
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; SEQ ID NO 2
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown NTP
; OTHER INFORMATION: peptide
US-10-198-070-2

Query Match 100.0%; Score 651; DB 14; Length 122;
Best Local Similarity 100.0%; Pred. No. 9.6e-70;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MMVCNRFKGVVYFISAIENFGPRYLHGVPFFYLILVRIISFLIGDMEDVLLNCTLLKR 60

Qy 61 SSRFRFGALVCSMDSCRSRVAVTYRFTILLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120
Db 61 SSRFRFGALVCSMDSCRSRVAVTYRFTILLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120

Qy 121 CL 122
Db 121 CL 122

RESULT 7

US-10-294-891-1
; Sequence 1, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK

; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-1

Query Match 100.0%; Score 651; DB 14; Length 122;
Best Local Similarity 100.0%; Pred. No. 9.6e-70;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVCNRFKGVVYFISAIENFGPRYLHGVPFFYLILVRIISFLIGDMEDVLLNCTLLKR 60
Db 1 MMVCNRFKGVVYFISAIENFGPRYLHGVPFFYLILVRIISFLIGDMEDVLLNCTLLKR 60

Qy 61 SSRFRFGALVCSMDSCRSRVAVTYRFTILLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120
Db 61 SSRFRFGALVCSMDSCRSRVAVTYRFTILLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120

Qy 121 CL 122
Db 121 CL 122

RESULT 8

US-10-920-313-1
; Sequence 1, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-1

Query Match 100.0%; Score 651; DB 17; Length 122;
Best Local Similarity 100.0%; Pred. No. 9.6e-70;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MMVCNRFKGVVYFISAIENFGPRYLHGVPFFYLILVRIISFLIGDMEDVLLNCTLLKR 60

Qy 61 SSRFRFGALVCSMDSCRSRVAVTYRFTILLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120
Db 61 SSRFRFGALVCSMDSCRSRVAVTYRFTILLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120

Qy 121 CL 122
Db 121 CL 122

RESULT 9

US-10-294-891-9

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; Sequence 9, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-9

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Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MMVCNRRFGKWVFI 15
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RESULT 10
US-10-920-313-9
; Sequence 9, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-9

Query Match      14.4%; Score 94; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MMVCNRRFGKWVFI 15
      |||||||

RESULT 11
US-10-294-891-10
; Sequence 10, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-10

Query Match      12.9%; Score 84; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 SAIFNFGPRYLXGV 30
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Db      1 SAIFNFGPRYLXGV 15
      |||||||

RESULT 12
US-10-920-313-10
; Sequence 10, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-10

Query Match      12.9%; Score 84; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 SAIFNFGPRYLXGV 30
      |||||||
Db      1 SAIFNFGPRYLXGV 15
      |||||||

RESULT 13
US-10-294-891-13
; Sequence 13, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-13

Query Match      12.7%; Score 83; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0092;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 61 SSRFRFWGALVCSMD 75
Db 1 SSRFRFWGALVCSMD 15
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1 IDQVLSRIKLEIKRCL 17
Db
Search completed: October 11, 2005, 07:39:42
Job time : 205.529 secs

RESULT 14
US-10-920-313-13
; Sequence 13, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GENMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-13
Query Match 12.7%; Score 83; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0092;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 61 SSRFRFWGALVCSMD 75
Db 1 SSRFRFWGALVCSMD 15
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RESULT 15
US-10-198-070-15
; Sequence 15, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GENMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-198-070-15
Query Match 12.6%; Score 82; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 106 IDQVLSRIKLEIKRCL 122
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:19 ; Search time 27.8904 Seconds
(without alignments)
326.535 Million cell updates/sec

Title: US-10-092-934-2
Perfect score: 651
Sequence: 1 MMVCNRFKQVVFISAFIN.....RNTIDQVLSRIKLEIKRCL 122

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	651	100.0	122	2	US-08-454-557C-40
2	651	100.0	122	2	US-08-340-426D-40
3	651	100.0	122	2	US-08-450-673C-40
4	651	100.0	122	5	PCT-US93-17111A-40
5	76	11.7	515	4	US-09-489-039A-12306
6	68.5	10.5	178	4	US-09-673-395A-330
7	68	10.4	233	4	US-09-886-319A-11
8	68	10.4	452	4	US-09-540-236-3030
9	67.5	10.4	222	1	US-07-732-242C-7
10	67	10.3	461	4	US-09-489-039A-9623
11	67	10.3	515	4	US-09-170-496D-104
12	66	10.1	515	4	US-09-170-496D-220
13	65.5	10.1	120	4	US-09-583-110-5022
14	65.5	10.1	122	4	US-09-107-433-3697
15	65.5	10.1	590	4	US-09-489-039A-8178
16	65	10.0	606	4	US-09-107-532A-4683
17	65	10.0	2596	4	US-09-949-016-9970
18	64.5	9.9	170	4	US-09-358-383C-27
19	64.5	9.9	341	4	US-09-270-767-45876
20	64.5	9.9	451	3	US-09-412-102-8
21	64.5	9.9	451	3	US-09-217-787-8
22	64.5	9.9	522	4	US-09-902-540-12872
23	64.5	9.9	832	4	US-09-206-551-21
24	64	9.8	352	4	US-09-495-406-22
25	64	9.8	352	4	US-09-816-028A-36
26	64	9.8	352	4	US-10-303-162-36
27	64	9.8	352	4	US-10-303-134-36

28	63.5	9.8	541	4	US-09-543-681A-4323	Sequence 4323, Ap
29	63	9.7	416	4	US-09-540-236-2393	Sequence 2393, Ap
30	63	9.7	434	4	US-09-543-681A-7154	Sequence 7154, Ap
31	63	9.7	623	4	US-09-252-991A-19867	Sequence 19867, A
32	62.5	9.6	453	4	US-09-743-742B-9	Sequence 9, Appli
33	62.5	9.6	453	4	US-09-825-294-209	Sequence 209, App
34	62.5	9.6	453	4	US-09-970-966-209	Sequence 209, App
35	62.5	9.6	1581	3	US-08-726-320-4	Sequence 4, Appli
36	62.5	9.6	1581	3	US-09-208-716-4	Sequence 4, Appli
37	62	9.5	160	4	US-09-107-532A-3836	Sequence 3836, Ap
38	62	9.5	233	4	US-09-148-545-137	Sequence 137, App
39	62	9.5	241	3	US-08-808-148-1	Sequence 1, Appli
40	62	9.5	241	3	US-09-020-956-114	Sequence 114, App
41	62	9.5	241	3	US-09-030-607-114	Sequence 114, App
42	62	9.5	241	3	US-09-439-313-114	Sequence 114, App
43	62	9.5	241	3	US-09-352-616A-114	Sequence 114, App
44	62	9.5	241	4	US-09-232-149A-114	Sequence 114, App
45	62	9.5	241	4	US-09-159-812-114	Sequence 114, App

ALIGNMENTS

RESULT 1
US-08-454-557C-40
; Sequence 40, Application US/08454557C
; Patent No. 5830670
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,557C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-454-557C-40

Query Match 100.0%; Score 651; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 6.3e-75;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MMVCNRFKQVVFISAFINFGPRYLXHGVPFFYLIVRIISFLIGMEDVLLNCTLKR 60
Db 1 MMVCNRFKQVVFISAFINFGPRYLXHGVPFFYLIVRIISFLIGMEDVLLNCTLKR 60
Oy 61 SSRFRFVGLVCSMDSCFRSFRVAVTYRFTLLNIPSPAVVMWNTIDQVLSRIKLETKR 120

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Db 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAARNTIDQQVLSRIKLEIKR 120
QY 121 CL 122
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Db 121 CL 122

RESULT 2
US-08-340-426D-40
; Sequence 40, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,426D
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-340-426D-40

Query Match 100.0%; Score 651; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 6.3e-75;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVCNRFQKVVYFISAIENFGPRYLYHGVPFFYLILVRIISFLIGDMEDVLLNCTLLKR 60
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Db 1 MMVCNRFQKVVYFISAIENFGPRYLYHGVPFFYLILVRIISFLIGDMEDVLLNCTLLKR 60
   |||

QY 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAARNTIDQQVLSRIKLEIKR 120
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Db 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAARNTIDQQVLSRIKLEIKR 120
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QY 121 CL 122
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Db 121 CL 122

RESULT 3
US-08-450-673C-40
; Sequence 40, Application US/08450673C
; Patent No. 5948888
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
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; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,673C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-450-673C-40

Query Match 100.0%; Score 651; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 6.3e-75;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MMVCNRFQKVVYFISAIENFGPRYLYHGVPFFYLILVRIISFLIGDMEDVLLNCTLLKR 60
   |||

QY 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAARNTIDQQVLSRIKLEIKR 120
   |||
Db 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAARNTIDQQVLSRIKLEIKR 120
   |||

QY 121 CL 122
   ||
Db 121 CL 122

RESULT 4
PCT-US95-17111A-40
; Sequence 40, Application PC/TUS9517111A
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
; TITLE OF INVENTION: Detection of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17111A
; FILING DATE:
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,426
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US95-17111A-40

Query Match 100.0%; Score 651; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 6.3e-75;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVCWNRFGKWVYFISAFNFGPRYLYHGVPFFYLILVRIISFLIGDMEDVLLNCTLLKR 60
Db 1 MMVCWNRFGKWVYFISAFNFGPRYLYHGVPFFYLILVRIISFLIGDMEDVLLNCTLLKR 60

Qy 61 SSRERFWGALVCSMDSCRFSSRVAVTYRFTLLNIPSPAVVMARNTIDQOVLRSIKLEIKR 120
Db 61 SSRERFWGALVCSMDSCRFSSRVAVTYRFTLLNIPSPAVVMARNTIDQOVLRSIKLEIKR 120

Qy 121 CL 122
Db 121 CL 122

RESULT 5
US-09-489-039A-12306
; Sequence 12306, Application US/09489039A
; Patent No. 8610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12306
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12306

Query Match 11.7%; Score 76; DB 4; Length 515;
Best Local Similarity 23.4%; Pred. No. 0.43;
Matches 28; Conservative 21; Mismatches 44; Indels 32; Gaps 6;

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Db 277 QWVRILLTLTLCNVCFGIRMAATWYVYTWNGQKHFPANLFTTLGVIGMIGSLAKVLT 336

Qy 55 ---CTLKRSRRFRFWGALVCSMDSCRF-----SRVAVTYRFTLLN-IPSPAVVMA 102
Db 337 DRWCKL-----QVFFWNIWLAVFSCAFYFNFPHATTLLIMLYFLLNHLHQIPSLHWSL 391

Qy 103 RNTID 107
Db 392 MSDVD 396

RESULT 6
US-09-673-395A-330
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; Sequence 330, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 330
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-395A-330

Query Match 10.5%; Score 68.5; DB 4; Length 178;
Best Local Similarity 35.2%; Pred. No. 1;
Matches 25; Conservative 11; Mismatches 22; Indels 13; Gaps 4;

Qy 8 FGKVVYFISAFNFGPRYLYHGVPFFYLILVRIISFLIGDMEDVLLNCTLL 58
Db 110 FGKVVYFVN--DFSFFFLCH-EPFLFLPLPFPVFSFLPLFPLSPVLUSLLCSCFSFL 165

Qy 59 KRSSRRFRFWGA 69
Db 166 RRSRIRLFCS 176

RESULT 7
US-09-886-319A-11
; Sequence 11, Application US/09886319A
; Patent No. 6586185
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
; TITLE OF INVENTION: Active Substances
; FILE REFERENCE: 50125/014002
; CURRENT APPLICATION NUMBER: US/09/886,319A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 10030149.5
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-886-319A-11

Query Match 10.4%; Score 68; DB 4; Length 233;
Best Local Similarity 25.6%; Pred. No. 1.7;
Matches 22; Conservative 14; Mismatches 22; Indels 28; Gaps 4;

Qy ...34 FLILVRIISFLIGDMEDVLLNCTLLKRSSRRFRFWGALVCSMDSCRFSSRVAVTYRFTLLN 93
Db 163 FIVLVPFVWFII--FKAYLINCV-----N-----NC-----YKVINRN 194

Qy 94 IPSPAVVMARNTIDQOVLRSIKLEIK 119
Db 94 IPSPAVVMARNTIDQOVLRSIKLEIK 119
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Db 195 VPEIAVPAPETPPQVVLPTYEMAVK 220

RESULT 8

US-09-540-236-3030

; Sequence 3030, Application US/09540236

; Patent No. 6673910

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS

; FILE REFERENCE: 2709.2005-001

; CURRENT APPLICATION NUMBER: US/09/540,236

; CURRENT FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 3840

; SEQ ID NO 3030

; LENGTH: 452

; TYPE: PRT

; ORGANISM: M.catarrhalis

US-09-540-236-3030

Query Match 10.4%; Score 68; DB 4; Length 452;

Best Local Similarity 26.5%; Pred. No. 3.8;

Matches 30; Conservative 14; Mismatches 43; Indels 26; Gaps 7;

QY 9 GKVVYFISAFN-----FGPR-----VLYHG-VPFYFLVRIISFLIGDM 48

Db 265 GRWFAVAVLTVVGLIMGIPFPQVVAEVTYLIAGTIVLYP--LYRFISPSLSKN 322

QY 49 EDV-LNCTLLKSSRRFRFGALVCSMDSCFRSRVAVTYRFTLLNIPSPAVW 100

Db 323 EKVRLLICFLIIGSTL-FWSSF--EQPTSFNLFADRYTDLNVMGFNIFSLW 372

RESULT 9

US-07-732-242C-7

; Sequence 7, Application US/07732242C

; Patent No. 5298399

; GENERAL INFORMATION:

; APPLICANT: Uozumi, Takeshi; Masaki, Haruhiko;

; APPLICANT: Hidaka, Makoto; Nakamura, Akira;

; APPLICANT: Maeda, Michihisa; Yoneta, Yasuo

; TITLE OF INVENTION: Gene of Urease

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Frishauf, Holtz, Goodman & Woodward, P.C.

; STREET: 600 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10016-2088

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 0.72mb

; COMPUTER: IBM PC compatible (NEC PC-9801 RX)

; OPERATING SYSTEM: MS DOS

; SOFTWARE: ASCII Form

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/732,242C

; FILING DATE: 19910718

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JPN 2-210178

; FILING DATE: 10-AUG-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Goodman, Herbert

; REGISTRATION NUMBER: 17081

; REFERENCE/DOCKET NUMBER: 910532/HG

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)972-1400

; TELEFAX: (212)370-1622

; TELE: 236268

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 222 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-07-732-242C-7

Query Match 10.4%; Score 67.5; DB 1; Length 222;

Best Local Similarity 26.7%; Pred. No. 1.8;

Matches 28; Conservative 12; Mismatches 34; Indels 31; Gaps 4;

QY 12 VYF-ISAIFNF-----GPRYLHGVFPFYFLVRIISFLIGDMEDVLLN 54

Db 88 VYFGISAILSLKKTTHESHRLHLDHPITYTKGIPYVKSFLGIHGLAGSAAMVLLT 147

QY 55 CTLKRRSR----FRFGALVCSMDSCFRSRVAVTYRFTLLNIP 95

Db 148 MSTVKAWEGLLYLFFGA-----GTVLGMLSFITLIGIP 182

RESULT 10

US-09-489-039A-9623

; Sequence 9623, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 9623

; LENGTH: 461

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-9623

Query Match 10.3%; Score 67; DB 4; Length 461;

Best Local Similarity 20.9%; Pred. No. 5.2;

Matches 24; Conservative 29; Mismatches 32; Indels 30; Gaps 5;

QY 29 GVPFYFLVRIISFLIGDMEDVLLNCTLLKSSRRFRPWG-----ALVCSM- 74

Db 43 GLPAYVYGLMFLVTRLVDGVADVLMLGLVIDNTTTR---WGRCRPWLILGALPGLLCILA 99

QY 75 -----DSCFRSRVAVTYRFTI---TLNIPSPAV--WMAWNTIDQOVLRSIKL 116

Db 100 FYVPDFGTTGKLLYAFVTYLCISFLYTLVNIPFCAMLPFLTSDSABRTLSAVRI 154

RESULT 11

US-09-170-496D-104

; Sequence 104, Application US/09170496D

; Patent No. 6555339

; GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-Coupled Receptors

; FILE REFERENCE: AREN-0040

; CURRENT APPLICATION NUMBER: US/09/170,496D

; CURRENT FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 294

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 104

; LENGTH: 515

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-170-496D-104

Query Match 10.1%; Score 67; DB 4; Length 515;
Best Local Similarity 22.1%; Pred. No. 6;
Matches 33; Conservative 23; Mismatches 49; Indels 44; Gaps 8;

QY 5 W-NRFGKWPYFISAIENFGPRYLHGVFPYFLILVR-----IIS 42
DB 196 WNSLGLHLVYVL--VYNITTVIVPVVVVFLILIRRLALSASOKKKVIAALRTPONTIS 253
QY 43 FLIGMEDVLLNCTLLKSSRFWFGALVCSMDSCRSRVAVTYRFTLLNIPS-----96
DB 254 IPYASQREAEHLATLLSMWVF-----ILCSVPYA---TLVVYQ--TVLNVPTSVFLL 302
QY 97 -PAVMARNTI--DQQVLSRIKLEIKRCL 122
DB 303 LTAVWLPKVSLLANPVLFLTVNKSVRKCL 331

RESULT 12
US-09-170-496D-220
; Sequence 220, Application US/09170496D
; Patent No. 655339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 655339--Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 220
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-220

Query Match 10.1%; Score 66; DB 4; Length 515;
Best Local Similarity 22.1%; Pred. No. 8;
Matches 33; Conservative 22; Mismatches 50; Indels 44; Gaps 8;

QY 5 W-NRFGKWPYFISAIENFGPRYLHGVFPYFLILVR-----IIS 42
DB 196 WNSLGLHLVYVL--VYNITTVIVPVVVVFLILIRRLALSASOKKKVIAALRTPONTIS 253
QY 43 FLIGMEDVLLNCTLLKSSRFWFGALVCSMDSCRSRVAVTYRFTLLNIPS-----96
DB 254 IPYASQREAEHLATLLSMWVF-----ILCSVPYA---TLVVYQ--TVLNVPTSVFLL 302
QY 97 -PAVMARNTI--DQQVLSRIKLEIKRCL 122
DB 303 LTAVWLPKVSLLANPVLFLTVNKSVRKCL 331

RESULT 13
US-09-583-110-5022
; Sequence 5022, Application US/09583110
; Patent No. 669703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02

; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 5022
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-5022

Query Match 10.1%; Score 65.5; DB 4; Length 120;
Best Local Similarity 28.8%; Pred. No. 1.6;
Matches 19; Conservative 9; Mismatches 17; Indels 21; Gaps 2;

QY 51 VLNCTLLKSSRFWFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVVMARNTIDQQV 110
DB 75 VLNCTPKVRQKSNFWSVHSTPDTRF-----FNFKDFL-----QLL 113
QY 111 LSRIKL 116
DB 114 LTHIKL 119

RESULT 14
US-09-107-433-3697
; Sequence 3697, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3697:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...122
; SEQUENCE DESCRIPTION: SEQ ID NO: 3697:
US-09-107-433-3697

Query Match 10.1%; Score 65.5; DB 4; Length 122;

```
Best Local Similarity 28.8%; Pred. No. 1.6;
Matches 19; Conservative 9; Mismatches 17; Indels 21; Gaps 2;

QY 51 VLLNCTLLKSSRFRFWGALVCSMDSCRSRVAVTYRFTLLNIPSPAVVMARNTIDQQV 110
Db 77 VLMNCTPKVQKSNFWSVHSTPDTRF-----FNKDFL-----QLL 115

QY 111 LSRKL 116
Db 116 LTHIKL 121

RESULT 15
US-09-489-039A-8178
; Sequence 8178, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; NUMBER OF SEQ ID NOS: 14342
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8178

Query Match 10.1%; Score 65.5; DB 4; Length 590;
Best Local Similarity 27.7%; Pred. No. 11;
Matches 38; Conservative 11; Mismatches 45; Indels 43; Gaps 7;

QY 2 MVCNRFQKVVYFISAFN-----FGPRVLY-----HGVPFFYLILVRIISFLIGD 47
Db 19 MVSW---GHWF---ALFNMLLAWVLGSRVLFVADWPTTLAQLRFSVSLVGHFSFL--- 68

QY 48 MEDVLLNCTLLKSSRFRFWGALVCSMDSCRSRVAVTYRFTLLNIPS----- 96
Db 69 ---VFTSYVLLIFPLTF-----IVSQRLMRFLSVILATAGMTLLLLIDSEVTRFHLN 120

QY 97 PAVVMARNTIDQQVLSR 113
Db 121 PVTWELVINPDQEMAR 137
```

Search completed: October 11, 2005, 07:42:46
Job time : 29.8904 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 17.369 Seconds
(without alignments)
620.432 Million cell updates/sec

Title: US-10-092-934-3
Perfect score: 570
Sequence: 1 MAQRLTATSASRVQAILLS.....GSCVVAQAGLKILASCNPSK 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 791:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	177	31.1	627	4 A40201	artifact-warning s
2	171	30.0	613	4 C40201	artifact-warning s
3	125.5	22.0	301	4 B40201	artifact-warning s
4	124.5	21.8	597	4 E40201	artifact-warning s
5	115	20.2	369	2 A33959	thromboxane A-2 re
6	111	19.5	619	2 A60646	transforming prote
7	98	17.2	673	4 F40201	artifact-warning s
8	97	17.0	107	2 C48078	biliary glycoprote
9	93	16.3	841	1 I78885	serine/threonine-s
10	90	15.8	579	4 D40201	artifact-warning s
11	88.5	15.5	499	2 S65657	alpha-1C-adrenergi
12	86	15.1	422	2 S23357	glial growth facto
13	84	14.7	125	2 S62676	heregulin isoform
14	83.5	14.6	125	2 I38405	neu differentiation
15	83.5	14.6	462	2 I38404	neu differentiation
16	83.5	14.6	640	2 A43273	heregulin precursor
17	82.5	14.5	639	2 I61719	neu differentiation
18	82	14.4	175	2 I38408	heregulin precursor
19	82	14.4	241	2 D43273	heregulin precursor
20	82	14.4	637	2 C43273	heregulin, splice
21	82	14.4	645	2 B43273	neu differentiation
22	81	14.2	230	2 A56210	neu differentiation
23	81	14.2	636	2 I61718	neu differentiation
24	81	14.2	662	2 I61722	neu differentiation
25	80.5	14.1	296	2 S32359	glial growth facto
26	80.5	14.1	296	2 A56943	sensory/motor neur
27	80	14.0	407	2 T02670	probable thromboxa
28	79.5	13.9	740	1 F0LJHD	gag polyprotein -
29	76	13.3	372	2 G01425	nucleolar 75K auto

30	75	13.2	79	2	A56194	thromboxane A-2 re
31	73	12.8	602	2	A45769	acetylcholine rece
32	72.5	12.7	513	2	T43179	probable dehydrata
33	72.5	12.7	598	2	T37858	probable dihydroxy
34	72.5	12.7	1964	2	T09059	notch4 - mouse
35	72	12.6	344	2	H45252	PilV constant regi
36	71.5	12.5	823	2	B87348	1,4-beta-D-glucan
37	71	12.5	385	2	E82317	D-erythrose 4-phos
38	70.5	12.4	1356	2	A45445	janusin precursor,
39	70	12.3	685	2	JC7570	Delta-4 protein -
40	69.5	12.2	394	2	E71136	threonine synthase
41	69.5	12.2	491	2	I45983	tyrosine 3-monooxy
42	69.5	12.2	907	2	S72765	phosphoenolpyruvat
43	69.5	12.2	934	2	B86981	probable phosphoen
44	69	12.1	100	2	A46010	X-linked retinopat
45	68.5	12.0	319	2	E82178	homoserine O-succi

ALIGNMENTS

RESULT 1
A40201
artifact-warning sequence (translated ALU class A) - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C:Accession: A40201
R:Claverie, J.M.
personal communication, 1992
A:Reference number: A40201
A:Accession: A40201
A:Molecule type: DNA
A:Residues: 1-627 <CLA>
R:Claverie, J.M.
Genomics 12, 838-841, 1992
A:Title: Identifying coding exons by similarity search: Alu-derived and other potentiall
A:Reference number: A40200; MUID:92241891; PMID:1572661
A:Contents: annotation
C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames of
in-frame stop codons are shown as 'X'.
C:Comment: Any significant similarity of a predicted protein sequence to a portion of th

Query Match	31.1%	Score 177;	DB 4;	Length 627;
Best Local Similarity	56.6%;	Pred. No. 1.1e-10;		
Matches	43;	Conservative	9;	Mismatches 22; Indels 2; Gaps 2;
Qy	1	MAQRLTATSASRVQAILLSOPKOLGRAPANTPLIFV-PSLEAGFHHICQAGLKLLTS	59	
Db	548	VARSRLTASSASRVHAILLPQPPKXGLQAPALRPANFLYFXRRGFTVARM-VSISXP	606	
Qy	60	GDPPASAFQSAGITGV	75	
Db	607	RDPALASQSAGITGV	622	

RESULT 2
C40201
artifact-warning sequence (translated ALU class C) - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C:Accession: C40201
R:Claverie, J.M.
personal communication, 1992
A:Reference number: A40201
A:Accession: C40201
A:Molecule type: DNA
A:Residues: 1-613 <CLA>
R:Claverie, J.M.
Genomics 12, 838-841, 1992
A:Title: Identifying coding exons by similarity search: Alu-derived and other potentiall
A:Reference number: A40200; MUID:92241891; PMID:1572661
A:Contents: annotation

C/Comment: This "warning" entry is a conceptual translation in all 6 reading frames of the sequence shown as 'X'.

A:Cross-references: 3069113330, OMIM:19310
A:Map position: 2p13-2p12
A:Introns: 214/1
C:Superfamily: rel transforming protein; rel homology
C:Keywords: DNA binding; nucleus; phosphoprotein; transcription regulation
F:8-296/Domain: rel homology <REL>
F:292-295/Region: nuclear location signal
F:267/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #stat


```

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: I78895
R/Levedakou, E.N.; He, M.; Baptist, E.W.; Craven, R.J.; Cance, W.G.; Welcsh, P.L.; Simmo
Oncogene 9, 1977-1988, 1994
A/Title: Two novel human serine/threonine kinases with homologies to the cell cycle regu
A/Reference number: I58396; MUID:94268838; PMID:8208544
A/Accession: I78895
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-841 <RES>
A/Cross-references: UNIPROT:P51957; GB:L20321; NID:G348244; PIDN:AAA36658.1; PID:G348245
C/Genetics:
A/Gene: GDB:STK2
A/Cross-references: GDB:374125
A/Map position: 3p21.1-3p21.1
C/Superfamily: human serine/threonine-specific protein kinase STK2; protein kinase homol
C/Keywords: phosphotransferase
F:4-261/Domain: protein kinase homology <KIN>

Query Match 16.3%; Score 93; DB 1; Length 841;
Best Local Similarity 33.0%; Pred. No. 0.1;
Matches 29; Conservative 10; Mismatches 33; Indels 16; Gaps 3;

Qy 14 VOAILSPQPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSGDPPASAFQSGAGIT 73
Db 444 LQPLIKEQPKDQSL---ALSP-----KLECSGTILAHNLRLGSGSDSPASASRVAGIT 495
Qy 74 GVSHLTQPNLDKKICNSGGSCYVAQAG 101
Db 496 GVCHHAQD-----QVAGECIIIEKQG 515

RESULT 10
D40201
artfact-warning sequence (translated ALU class D) - human
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C/Accession: D40201
R/Claverie, J.M.
personal communication, 1992
A/Reference number: A40201
A/Accession: D40201
A/Molecule type: DNA
A/Residues: 1-579 <CLA>
R/Claverie, J.M.
Genomics 12, 838-841, 1992
A/Title: Identifying coding exons by similarity search: Alu-derived and other potentiall
A/Reference number: A40200; MUID:92241891; PMID:1572661
A/Contents: annotation
C/Comment: This "warning" entry is a conceptual translation in all 6 reading frames of o
in-frame stop codons are shown as 'X'.
C/Comment: Any significant similarity of a predicted protein sequence to a portion of th

Query Match 15.8%; Score 90; DB 4; Length 579;
Best Local Similarity 45.7%; Pred. No. 0.14;
Matches 21; Conservative 9; Mismatches 14; Indels 2; Gaps 1;

Qy 15 QAILLSQPKQLGLRAPANTP--LIFVFSLEAGFHHCQAGLKLLT 58
Db 416 QVILLPQPFEXLGLQAYATRSGLFYLFYFVEVGFRRHVAQAVLELLS 461

RESULT 11
S65657
alpha-1C-adrenergic receptor splice form 2 - human
N/Alternate names: alpha-1C-adrenoceptor isoform 2
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C/Accession: S65657; S65655
R/Tanaka, T.
submitted to the EMBL Data Library, July 1994
A/Reference number: S65656

```


Qy 62 PPASAFOSAGITGVSHLTOPANLDKIKCSNGGSCVVAQ---AGLKLLASCNP 110
Db 164 -NTSSSTSTTGTSHLVKCAEKEKTCVNGGECFMVADLSNPSRYLCKCQP 214

Search completed: October 11, 2005, 07:01:34
Job time : 19.369 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 67.2299 Seconds
(without alignments)
853.085 Million cell updates/sec

Title: US-10-092-934-3

Perfect score: 570

Sequence: 1 MAQSRLTATSASRVQAILLS.....GSCVVAQAGLKLASCNPFSK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	232.5	40.8	133	Q6ZQZ5	Q6zqz5 homo sapien
2	223.5	39.2	184	Q6ZW29	Q6zw29 homo sapien
3	214.5	37.6	123	Q9HAD8	Q9had8 homo sapien
4	208	36.5	174	Q8N2A0	Q8n2a0 homo sapien
5	205	36.0	139	Q6ZVJ8	Q6zvj8 homo sapien
6	201.5	35.4	587	ALU3 HUMAN	P39190 homo sapien
7	201	35.3	239	Q6ZWA9	Q6zwa9 homo sapien
8	201	35.3	585	ALU5 HUMAN	P39192 homo sapien
9	200.5	35.2	587	ALU2 HUMAN	P39189 homo sapien
10	200	35.1	138	Q6ZR23	Q6zr23 homo sapien
11	200	35.1	138	Q6ZVB3	Q6zvb3 homo sapien
12	198	34.7	109	Q8NI81	Q8ni81 homo sapien
13	191.5	33.6	188	Q6ZQN4	Q6zqn4 homo sapien
14	187	32.8	593	ALU7 HUMAN	P39194 homo sapien
15	184	32.3	202	Q6ZUA4	Q6zua4 homo sapien
16	183	32.1	128	Q6ZPB2	Q6zpb2 homo sapien
17	181.5	31.8	603	ALU4 HUMAN	P39191 homo sapien
18	181	31.8	133	Q6ZJR5	Q6zjr5 homo sapien
19	181	31.8	155	Q6ZSW8	Q6zsw8 homo sapien
20	181	31.8	222	Q6ZU09	Q6zu09 homo sapien
21	180	31.6	146	Q6ZTX8	Q6ztx8 homo sapien
22	179	31.4	174	Q9H926	Q9h926 homo sapien
23	178.5	31.3	164	Q6ZTS0	Q6zts0 homo sapien
24	177	31.1	124	Q6ZUN5	Q6zun5 homo sapien
25	176	30.9	118	Q9H387	Q9h387 homo sapien
26	175	30.7	115	Q9N083	Q9n083 macaca fasc
27	174	30.5	140	Q8N891	Q8n891 homo sapien
28	173.5	30.4	169	Q9H397	Q9h397 homo sapien
29	173	30.4	140	Q6ZP99	Q6zp99 homo sapien
30	173	30.4	164	Q6ZUK0	Q6zuk0 homo sapien
31	172.5	30.3	138	Q6ZUF3	Q6zuf3 homo sapien

32	172.5	30.3	179	2	Q8N1K7	Q8n1k7 homo sapien
33	172	30.2	123	2	Q6ZTE8	Q6zte8 homo sapien
34	172	30.2	125	2	Q6ZTE1	Q6zte1 homo sapien
35	172	30.2	593	1	ALU6 HUMAN	P39193 homo sapien
36	171.5	30.1	171	2	Q9H728	Q9h728 homo sapien
37	170.5	29.9	150	2	Q6ZPA0	Q6zpa0 homo sapien
38	170.5	29.9	156	2	Q6ZUA3	Q6zua3 homo sapien
39	170	29.8	101	2	Q6STG2	Q6stg2 homo sapien
40	170	29.8	125	2	Q6ZTC7	Q6ztc7 homo sapien
41	170	29.8	156	2	Q8NBH4	Q8nbh4 homo sapien
42	170	29.8	204	2	Q8N8P8	Q8n8p8 homo sapien
43	169.5	29.7	148	2	Q6ZUC5	Q6zuc5 homo sapien
44	169.5	29.7	170	2	Q8NAI3	Q8nai3 homo sapien
45	168.5	29.6	224	2	Q8N2I0	Q8n2i0 homo sapien

ALIGNMENTS

RESULT 1

ID Q6ZQZ5 PRELIMINARY; PRT; 133 AA.
AC Q6ZQZ5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ46775.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Trachea;
RA Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
RA Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,
RA Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK128616; BAC87531.1;
SQ SEQUENCE 133 AA; 14947 MW; 3A349D8E39D62D3C CRC64;

Query Match 40.8%; Score 232.5; DB 2; Length 133;

Best Local Similarity 68.5%; Pred. No. 6.3e-16;

Matches 50; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

Qy 10 SASRVQAILLSOPPKQLGLRAPANTP-LIFVFSLEAGFHHCQAGLKLTSGLDPPASAFQ 68
Db 42 TASQVQAILLTQPKWLGLRAYATAPGYFFVLVEIGHVHVRPGLKLTSGDPPALASQ 101

Qy 69 SAGITGVSHLTQP 81

Db 102 GAGIAGVSHRTWP 114

RESULT 2

ID Q6ZW29 PRELIMINARY; PRT; 184 AA.
AC Q6ZW29;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein FLJ41703.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Heart;


```

QY 65 SAFOSAGITGVSHLTQANLDDKKICNSGGSCYVAQAG 101
DB 149 SASOSAGITGVSHSARPK-----SCFLQLLG 174

RESULT 5
Q6ZVJ8
ID Q6ZVJ8 PRELIMINARY; PRT; 139 AA.
AC Q6ZVJ8 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ42505.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Iehii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Puji A., Oshima A., Suzuki Y.,
RA Sugano S., Nagahari K., Maehuo Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK12496; BAC95863.1; -
SQ SEQUENCE 139 AA; 15636 MW; 92C7CF6C06316811 CRC64;

Query Match 36.0%; Score 205; DB 2; Length 139;
Best Local Similarity 55.2%; Pred. No. 4.3e-13;
Matches 48; Conservative 11; Mismatches 22; Indels 6; Gaps 1;

QY 1 MAQSRLTATSASRVQAILLSQPPKQLGRAPANTP-----LIFVFSLEAGFHHICQAGL 54
DB 41 VARSRLTETSASRIQAILLSRPSRWLGLQACATWPGYLVVVVVLLVETMFLHFGQAGL 100

QY 55 KLLTSGDPPASAFOSAGITGVSHLTQ 81
DB 101 ELLTSGDPPASASQSTGITRMRDAQP 127

RESULT 6
ALU3 HUMAN STANDARD; PRT; 587 AA.
AC P39190;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alu subfamily SBI sequence contamination warning entry.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.; Makalowski W.;
RT "Alu alert.";
RL Nature 371:752-752(1994).
RN [2]
RP CONCEPT.
RX MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.;
RT "Identifying coding exons by similarity search: alu-derived and other
potentially misleading protein sequences.";
RL Genomics 12:838-841(1992).
RN [3]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA Quentini Y.;
RT "The Alu family developed through successive waves of fixation closely

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RT connected with primate lineage history.";
RN J. Mol. Evol. 27:194-202(1988).
RX [4]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J., Milosavljevic A.;
RT "Reconstruction and analysis of human Alu genes.";
RN J. Mol. Evol. 32:105-121(1991).
CC -!- MISCELLANEOUS: Various analyses indicate that Alu repeats fall
into 8 subfamilies (Ref.3 and Ref.4). Therefore, 8 Alu warning
consensus sequences have been constituted that contain all six
frames conceptual translations of each of these classes of Alu
repeats.
CC -!- MISCELLANEOUS: Isolated 'X' indicates the presence of a stop
codon, 'XXX' is used to separate the various translation phases.
CC -!- CAUTION: This Alu entry is provided in order to avoid the further
pollution of protein sequence databases with Alu-derived amino
acid sequences.
CC -!- CAUTION: Alu repetitive sequences are interspersed in human and
primate genomes with an average spacing of 4 kb. Some of them are
actively transcribed by pol III. Normal transcripts may contain
Alu-derived sequences in 5' or 3' untranslated regions. However,
cDNA libraries also contain partial and/or rearranged cDNAs
ligated with Alu-derived sequence in any orientation. Although Alu
elements (especially situated on the complementary strand) have a
great potential to create additional/alternative exons,
consideration should be given to the possibility that the presence
of an Alu in an open reading frame may have resulted from a
cloning artifact or may be due to misinterpretation of sequencing
data. This point has been overlooked on several occasions, with
the consequence of erroneous Alu-derived amino acid sequences
being reported.
CC -!- CAUTION: Any significant similarity of a putative protein sequence
with an Alu-translated entry must be taken as a warning that a
part of Alu repeat may have been artifactually included in the
coding nucleotide sequence.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U14569; -; NOT_ANNOTATED_CDS.
KW Hypothetical protein.
FT DOMAIN 1 96 Frame-1.
FT DOMAIN 100 194 Frame-2.
FT DOMAIN 198 292 Frame-3.
FT DOMAIN 296 391 Frame-4.
FT DOMAIN 395 489 Frame-5.
FT DOMAIN 493 587 Frame-6.
SQ SEQUENCE 587 AA; 63573 MW; 85C4155726DEF235 CRC64;

Query Match 35.4%; Score 201.5; DB 1; Length 587;
Best Local Similarity 52.4%; Pred. No. 4.7e-12;
Matches 55; Conservative 11; Mismatches 30; Indels 9; Gaps 4;

QY 1 MAQSRLTATSASRVQAILLSQPPKQLGRAPANTPLIFV-PSLEAGFHHICQAGL-KLLT 58
DB 410 VAGSRLTASSASRVHAILLPQPKXGLQADATTPGFLFYXRRGFTVL--AGWVSIX 467

QY 59 SGDPFPASAFOSAGITGVSHLTQANLDDKKICNSGGSCYVAQAGLK 103
DB 468 PRDPFPASASQAGITGVSHRAXXXFFET-----ESRSVAQAGVQ 507

RESULT 7
Q6ZWA9 PRELIMINARY; PRT; 239 AA.
ID Q6ZWA9
AC Q6ZWA9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

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RA	Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., WA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., RA Suzuki Y., Sugano S., Nagahari K., Masuko Y., Nagai K., Isogai T.; RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases. DR EMBL; AK124786; BAC65949.1; -- SQ SEQUENCE 138 AA; 14947 MW; D0538C4BB90C9E2C CRC64;
Query Match 35.1%; Score 200; DB 2; Length 138; Best Local Similarity 50.5%; Pred. No. 1.4e-12; Matches 56; Conservative 13; Mismatches 24; Indels 18; Gaps 5;	
Qy	1 MAQSRLTATSRSRVOAILLSOPPKQLGLRAPANTPLIFVFSLEAGFHHICOAGLKLLTSG 60 : : : Db 34 VVRSWLTATSAQSIVAGI-----TGMMHHAQ--LIPFLVENGFHCVCVGAGLELLTSG 83 : : :
Qy	61 DPPASAFOSAGITGVSHLTGPANLDKKICNSNG--SCVVAQA---GKILIA 106 : : :
Dd	84 DPPASAQSSAGIIIGVSHCTRP--NFCISFRDGVSPCWLSWSGTGHKLSLA 131 : : : : : : ~~~~~~ :
RESULT 12	
QBNI81	PRELIMINARY; PRT; 109 AA.
ID QBNI81	
AC QBNI81	
DT 01-OCT-2002 (TrEMBLrel. 22, Created)	
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)	
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)	
DE OK/SW-CL.41.	
GN Name=OK/SW-cl.41;	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RA Shichijo S., Itoh K.; RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases. DR EMBL; AB062477; BAB93502.1; -- SQ SEQUENCE 109 AA; 11580 MW; FB5200153CEE2B33 CRC64;	
Query Match 34.7%; Score 198; DB 2; Length 109; Best Local Similarity 61.6%; Pred. No. 1.7e-12; Matches 45; Conservative 4; Mismatches 14; Indels 10; Gaps 8;	
Qy	9 TSASRVQAILLSOPPKQLGLRAPANTPLIFVFSLEAGFHHICOAGLKLLTSGDPASAFO 68 : Dd 31 TSASRVAGITGMQ-----HTTLQILFLVLVMGFHFHVQGAGLKLLTSGDPASASQ 80 : : :
Qy	69 SAGITGVSHLTQP 81 :
Dd	81 SAGITGVGHHTWP 93 :
RESULT 13	
QEQZNA	PRELIMINARY; PRT; 188 AA.
ID QEQZNA	
AC QEQZNA	
DT 05-JUL-2004 (TrEMBLrel. 27, Created)	
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
DE Hypothetical protein FLJ46832.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE=Uterus;	
RA Nimomiyama K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Fujiya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R., RA Otsuki T., Saito H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,	

ligated with Alu-derived sequence in any orientation. Although Alu elements (especially situated on the complementary strand) have a great potential to create additional/alternative exons, consideration should be given to the possibility that the presence of an Alu in an open reading frame may have resulted from a cloning artifact or may be due to misinterpretation of sequencing data. This point has been overlooked on several occasions, with the consequence of erroneous Alu-derived amino acid sequences being reported.

-!- CAUTION: Any significant similarity of a putative protein sequence with an Alu-translated entry must be taken as a warning that a part of Alu repeat may have been artifactually included in the coding nucleotide sequence.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 82.9519 Seconds
(without alignments)
522.196 Million cell updates/sec

Title: US-10-092-934-3

Perfect score: 570

Sequence: 1 MAQSRLTATSASRVQAILLS.....GSCVVAQAGLKLASCNPSK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq16Dec04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	570	100.0	112	5 AAE29144	Neural th
2	570	100.0	112	6 ABP59925	Human 112
3	570	100.0	112	6 AAE33191	Neural th
4	570	100.0	112	7 ADL96023	Human neu
5	565	99.1	112	6 ABR63242	112 amino
6	565	99.1	112	6 ABU02974	Human neu
7	565	99.1	112	6 ABJ19447	112-mer n
8	565	99.1	112	7 ADB37521	Neural th
9	282.5	49.6	170	7 ADC86487	Human GPC
10	251.5	44.1	151	7 ADC86543	Human GPC
11	240	42.1	160	7 ADC86547	Human GPC
12	232.5	40.8	133	8 ADR10295	Human pro
13	230.5	40.4	109	7 ADM03914	Human pro
14	227.5	39.9	80	5 AAE20824	Human gen
15	227.5	39.9	80	5 AAE20801	Human gen
16	227.5	39.9	80	5 ABG64654	Human alb
17	227.5	39.9	80	5 ABG64656	Human alb
18	227.5	39.9	80	8 ADL77923	Albumin f
19	227.5	39.9	80	8 ADL77921	Albumin f
20	226.5	39.7	104	6 ABP60670	Steroid t
21	226.5	39.7	200	7 ADC86585	Human GPC
22	223.5	39.2	184	8 ADQ65893	Novel hum
23	219	38.4	397	2 AAR95913	Neural th
24	216	37.9	276	4 ABG07919	Novel hum
25	215.5	37.8	138	4 AAM24396	Human EST

ALIGNMENTS

RESULT 1

AAE29144
ID AAE29144 standard; protein; 112 AA.

XX AAE29144;
AC AAE29144;

XX 27-JAN-2003 (first entry)
DT 27-JAN-2003 (first entry)

XX Neural thread protein (NTP) #2.
DE Neural thread protein (NTP) #2.

XX Neural thread protein; NTP; hyperplasia; hypertrophy; arteriosclerosis;
KW haemorrhoid; gene therapy; tumour; vascular disease; atherosclerosis;
KW inflammatory disease; nutritional deficiency disease; genetic disease;
KW autoimmune disease; metabolic disease; traumatic disease; intoxication;
KW infectious disease; congenital malformation; enzyme deficiency disease;
KW amyloid disease; fibrosis disease; storage disease; radiation disease;
KW poisoning; environmental disease; endocrine disease; protein therapy;
KW degenerative disease; mechanical disease.

XX Unidentified.

OS WO200274323-A2.
XX WO200274323-A2.

XX 26-SEP-2002.
PD 26-SEP-2002.

XX 08-MAR-2002; 2002WO-IB001959.
PF 08-MAR-2002; 2002WO-IB001959.

XX 08-MAR-2001; 2001US-0273957P.
PR 08-MAR-2001; 2001US-0273957P.

XX (AVER/) AVERBACK P.
PA (AVER/) AVERBACK P.

XX AVERBACK P;
PI AVERBACK P;

XX WPI; 2002-759864/82.
DR WPI; 2002-759864/82.

XX Treating a condition in a patient requiring removal or destruction of
PT cells, such as a benign or malignant tumor of a tissue or an inflammatory
PT disease, comprises administering a neural thread protein (NTP) or a NTP
PT gene to a mammal.

XX Claim 23; Fig 3; 70pp; English.
PS Claim 23; Fig 3; 70pp; English.

XX The invention relates to a method for treating a condition in a patient
XX requiring removal or destruction of cells. The method involves
CC administering to a mammal a neural thread protein (NTP), or administering
CC to a tumour or other target cell a NTP gene, where the expression of the
CC NTP gene is induced resulting in expression of the NTP protein. The
CC method and NTP are useful for treating a condition in a patient requiring

Aab944974 Human pro
Adb37562 Neural th
Aae07113 Human gen
Adb64029 Human pro
Aam23681 Human EST
Adg65120 Novel hum
Abj18397 Breast sp
Adg65417 Novel hum
Aam82366 Human imm
Adm04871 Human pro
Adg65405 Novel hum
Adr10238 Human pro
Adc86933 Human GPC
Adc87053 Human GPC
Add22434 HLA-B*45 T
Adi15930 Human PP
Adb64756 Human pro
Aao07175 Human pol
Adr09436 Human pro

26 214.5 37.6 123 4 AAB94974
27 214.5 37.6 123 7 ADB37562
28 212.5 37.3 164 4 AAE07113
29 208 36.5 174 7 ADB64029
30 207.5 36.4 87 4 AAM23681
31 205 36.0 139 8 ADG65120
32 204.5 35.9 116 6 ABJ18397
33 201 35.3 239 8 ADG65417
34 200 35.1 103 4 AAM82366
35 200 35.1 138 7 ADM04871
36 200 35.1 138 8 ADG65405
37 200 35.1 138 8 ADR10238
38 199 34.9 161 7 ADC86933
39 198.5 34.8 156 7 ADC87053
40 198 34.7 109 7 ADD22434
41 198 34.7 109 7 ADI15930
42 195.5 34.3 122 7 ADB64756
43 195 34.2 113 7 ADB64756
44 195 34.2 130 4 AAO07175
45 194 34.0 115 8 ADR09436

CC removal or destruction of cells, such as a benign or malignant tumour of
CC a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue,
CC preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,
CC bacterially, or parasitically altered tissue, or a malformation of a
CC tissue. Other conditions include a cosmetic modification to a tissue,
CC such as removal of unwanted facial hair, warts or unwanted fatty tissue,
CC a vascular disease, particularly atherosclerosis or arteriosclerosis,
CC haemorrhoids, or varicose veins, an inflammatory disease, autoimmune
CC or physical injury, nutritional deficiency disease, infectious disease,
CC congenital malformation, amyloid disease, fibrosis disease, storage
CC disease, enzyme deficiency disease, poisoning, intoxication, degenerative
CC disease, radiation disease, environmental disease, endocrine disease or
CC mechanical disease. The invention is useful in protein therapy and gene
CC therapy. The present sequence is NTP protein
XX
SQ Sequence 112 AA;

Query Match 100.0%; Score 570; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 2e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAOSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHICQAGLKLTSG 60
Db 1 MAOSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHICQAGLKLTSG 60
QY 61 DPASAFQSAGITGVSHLTQPANLDKKKICSGGSCYVAQAGLKLLASCNPSK 112
Db 61 DPASAFQSAGITGVSHLTQPANLDKKKICSGGSCYVAQAGLKLLASCNPSK 112

RESULT 2
ABP59925

ID ABP59925 standard; protein; 112 AA.

AC ABP59925;

XX 08-SEP-2003 (first entry)

DT Human 112 amino acid neural thread protein.

DE
XX Human; tumour; cancer; neural thread protein; NTP; cell removal;
KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;
KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;
KW gene therapy.

XX Homo sapiens.

XX WO2003044053-A2.

XX 30-MAY-2003.

XX 18-NOV-2002; 2002WO-CA001757.

XX 16-NOV-2001; 2001US-0331477P.

XX (NYMO-) NYMOX CORP.

XX Averbach P, Gemmell J;

XX WPI; 2003-457592/43.

XX New neural thread protein (NTP), useful for preparing a composition for
PT treating or preventing a condition in a mammal requiring removal or
PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or
PT inflammatory disease.

XX Disclosure; Fig 2; 98pp; English.

XX The present invention relates to peptides derived from the human neural
CC thread protein (NTP). The peptides are useful for preparing a composition
CC for treating or preventing a condition in a mammal requiring removal or
CC destruction of cells, comprising tonsillary hypertrophy, prostatic

CC hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a
CC breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,
CC varicose veins, atherosclerosis, inflammatory, metabolic, infectious,
CC fibrosis, endocrine or autoimmune disease, or stenosis, restenosis, in
CC occlusion or blockage of an artery or of a stent placed or implanted in
CC an artery. The present sequence is an NTP protein used to produce
CC peptides of the invention
XX

SQ Sequence 112 AA;

Query Match 100.0%; Score 570; DB 6; Length 112;
Best Local Similarity 100.0%; Pred. No. 2e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAOSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHICQAGLKLTSG 60
Db 1 MAOSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHICQAGLKLTSG 60

QY 61 DPASAFQSAGITGVSHLTQPANLDKKKICSGGSCYVAQAGLKLLASCNPSK 112

Db 61 DPASAFQSAGITGVSHLTQPANLDKKKICSGGSCYVAQAGLKLLASCNPSK 112

RESULT 3

AAE33191

ID AAE33191 standard; protein; 112 AA.

XX AAE33191;

XX 16-APR-2003 (first entry)

DT Neural thread protein (NTP) #2.

DE
XX Cell death; tissue necrosis; neural thread protein; NTP; amyloidosis;
KW stroke; brain tumour; Pick's disease; Parkinson's disease; glaucoma;
KW Alzheimer's disease; gene therapy.

XX Unidentified.

XX WO200289841-A2.

XX 14-NOV-2002.

XX 06-MAY-2002; 2002WO-CA000681.

XX 04-MAY-2001; 2001US-0288463P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-120506/11.

XX Preventing, controlling, modulating, ameliorating and/or treating cell
PT death or tissue necrosis using antibodies to neural thread proteins,
PT useful in disorders such as stroke, brain tumor, glaucoma and Alzheimer's
PT disease.

XX Disclosure; Fig 6; 60pp; English.

XX The invention relates to a method of preventing, and/or inhibiting cell
CC death and/or tissue necrosis in live tissue containing neural thread
CC proteins (NTP). The method involves contacting the live tissue with at
CC least one antibody, fragment or derivative that recognises NTP, where the
CC antibody, fragment or derivative is present to prevent, control,
CC ameliorate and/or inhibit cell death and/or tissue necrosis caused by the
CC presence of NTP. Methods and compositions of the invention are useful for
CC preventing, modulating, controlling and/or treating disorders associated
CC with cell death and/or tissue necrosis such as stroke, brain tumour,
CC Pick's disease, Parkinson's disease, amyloidosis, glaucoma and
CC Alzheimer's disease. The invention is useful in gene therapy. The present
CC sequence is NTP protein
XX

CC	tumours and other conditions requiring the removal or destruction of
CC	cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or
CC	atherosclerosis). These may also be used in treating inflammatory
CC	diseases, autoimmune diseases, metabolic diseases, hereditary/genetic
CC	diseases, traumatic diseases or physical injuries, nutritional deficiency
CC	diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,
CC	storage diseases, congenital malformation, enzyme deficiency diseases,
CC	poisoning, intoxication, environmental diseases, radiation diseases,
CC	endocrine diseases, degenerative diseases or mechanical diseases. The
CC	present sequence is a human NTP protein from which the peptides of CC
CC	invention are derived.
XX	
SQ	Sequence 112 AA;
	Query Match 100.0%; Score 570; DB 7; Length 112;
	Best Local Similarity 100.0%; Pred. No. 2e-57;
	Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 MAQSRLTATSASRVQAILLISOPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLLTSG 60
DB	1 MAQSRLTATSASRVQAILLISOPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLLTSG 60
QY	61 DPPASAFQAGITGVSHLTLPANLDDKKICNSGGSCYYAQAQGLKLLASCNP SK 112
DB	61 DPPASAFQAGITGVSHLTLPANLDDKKICNSGGSCYYAQAQGLKLLASCNP SK 112
RESULT 5	
ABR63242	
ID	ABR63242 standard; protein; 112 AA.
XX	
AC	ABR63242;
XX	
DT	28-AUG-2003 (first entry)
XX	
DE	112 amino acid neural thread protein.
XX	
KW	Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW	neural thread protein; NTP; tumour.
XX	
OS	Unidentified.
XX	
FN	WO2003008443-A2.
XX	
PD	30-JAN-2003.
XX	
PF	19-JUL-2002; 2002WO-COA01105.
XX	
PR	19-JUL-2001; 2001US-0306150P.
XX	
PR	19-JUL-2001; 2001US-0306161P.
XX	
PR	16-NOV-2001; 2001US-0331477P.
XX	
PA	(NYMO-) NYMOX CORP.
XX	
PI	Averback PA;
XX	
DR	WIPI; 2003-247999/24.
XX	
PT	Novel neural thread protein peptide, referred as cell death peptide,
PT	useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
PT	atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
XX	
PS	Disclosure; Fig 3; 77pp; English.
XX	
CC	The present invention relates to a neural thread protein (NTP) peptide
CC	referred to as cell death peptide. Thought to be cytostatic,
CC	antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC	treating a condition in a patient requiring removal or destruction of
CC	cells, for treating a condition such as benign or malignant tumor,
CC	inflammatory disease, autoimmune disease and infectious disease. The
CC	peptide useful for treatment is derived from the amino acid sequence for
CC	a pancreatic thread protein. The peptide is conjugated, linked or bound
CC	to a molecule chosen from antibody or its fragment, antibody-like binding

CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side
CC effects of surgery. The present sequence is an NTP amino acid sequence
XX
SQ Sequence 112 AA;
Query Match 99.1%; Score 565; DB 6; Length 112;
Best Local Similarity 99.1%; Pred. No. 7.6e-57;
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAQSRLTATSASRVOAILLSQPPKQLGLRAPANTPLIFVFSLEAGPHHICQAGLKLLTSG 60
DB 1 MAQSRLTATSASRVOAILLSQPPKQLGLRAPANTPLIFVFSLEAGPHHICQAGLKLLTSG 60
QY 61 DPPASAFQSAGITGVSHLTQPNALDKKICSNNGSCYVAQAGLKLLASCNPSK 112
DB 61 DPPASAFQSAGITGVSHLTQPNALDKKICSNNGSCYVAQAGLKLLASCNPSK 112
RESULT 6
ABU02974
ID ABU02974 standard; protein; 112 AA.
AC ABU02974;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human neural thread protein AD7C-NTP, protein fragment #2.
XX
KW Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;
KW transplantation; grafting; chemotherapy; immunotherapy; vaccination;
KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;
KW radiation; tumor; hyperplasia; hypertrophy; overgrowth of tissue;
KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;
KW cosmetic modification; vascular disease; atherosclerosis;
KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;
KW autoimmune disease; metabolic disease; traumatic disease;
KW physical injury; nutritional deficiency disease; infectious disease;
KW amyloid disease; fibrosis disease; storage disease;
KW congenital malformation; enzyme deficiency disease; poisoning;
KW intoxication; environmental disease; radiation disease;
KW endocrine disease; degenerative disease; mechanical disease.
XX
OS Homo sapiens.
XX
PN WO200297030-A2.
XX
PD 05-DEC-2002.
XX
PF 24-MAY-2002; 2002WO-CA000759.
XX
PR 25-MAY-2001; 2001US-0293156P.
XX
PA (NYMO-) NYMOX CORP.
XX
PI Averbach PA;
XX
DR WPI; 2003-041406/03.
XX
PT Novel peptides similar in amino acid sequence to neural thread proteins
PT (NTP), useful for treating unwanted cellular proliferations such as
PT malignant tumors and prostatic hyperplasia.
PS
PS Disclosure; Fig 3; 78pp; English.
XX
CC The invention describes an NTP-peptide (I) comprising at least one amino
CC acid sequence corresponding to part of the amino acid sequence of a
CC neural thread protein, AD7C-NTP. The invention provides a method of
CC treating a condition requiring removal or destruction of cells of a
CC mammal comprising administering to a mammal, a therapeutic amount of (I).
CC The treatment is administered to the mammal before, during or after
CC surgical excision, transplantation, grafting, chemotherapy.

CC immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,
CC laser therapy, phototherapy, gene therapy and/or radiation. The method is
CC useful for treatment of benign or malignant tumour; hyperplasia,
CC hypertrophy or overgrowth of tissue; virally, bacterially or
CC parasitically altered tissue; malformation of tissue selected from lung,
CC breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,
CC sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary
CC gland, blood, brain and its coverings, spinal cord, muscle, connective
CC tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary,
CC reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,
CC tonsils, mouth and lymph nodes and lymphoid system; tonsillary
CC hypertrophy; prostatic hyperplasia; cosmetic modification to a tissue;
CC vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;
CC varicose veins; inflammatory disease; autoimmune disease; metabolic
CC disease; hereditary/genetic disease; traumatic disease; physical injury;
CC nutritional deficiency disease; infectious disease; amyloid disease;
CC fibrosis disease; storage disease; congenital malformation; enzyme
CC deficiency disease; poisoning; intoxication; environmental disease;
CC radiation disease; endocrine disease; degenerative disease and mechanical
CC disease. This is the amino acid sequence of a human neural thread protein
CC AD7C-NTP protein fragment
XX
SQ Sequence 112 AA;
Query Match 99.1%; Score 565; DB 6; Length 112;
Best Local Similarity 99.1%; Pred. No. 7.6e-57;
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAQSRLTATSASRVOAILLSQPPKQLGLRAPANTPLIFVFSLEAGPHHICQAGLKLLTSG 60
DB 1 MAQSRLTATSASRVOAILLSQPPKQLGLRAPANTPLIFVFSLEAGPHHICQAGLKLLTSG 60
QY 61 DPPASAFQSAGITGVSHLTQPNALDKKICSNNGSCYVAQAGLKLLASCNPSK 112
DB 61 DPPASAFQSAGITGVSHLTQPNALDKKICSNNGSCYVAQAGLKLLASCNPSK 112
RESULT 7
ABJ19447
ID ABJ19447 standard; protein; 112 AA.
XX
AC ABJ19447;
XX
DT 27-MAR-2003 (first entry)
XX
DE 112-mer neural thread protein.
XX
KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.
XX
OS Unidentified.
XX
PN WO200292115-A2.
XX
PD 21-NOV-2002.
XX
PF 16-MAY-2002; 2002WO-CA000712.
XX
PR 16-MAY-2001; 2001US-0290971P.
XX
PA (NYMO-) NYMOX CORP.
XX
PI Averbach PA;
XX
DR WPI; 2003-129234/12.
XX
PT Preventing and/or inhibiting cell death and/or tissue necrosis in a
PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
PT disease, by contacting the live tissue with at least one segment of
PT neural thread proteins (NTP).
XX
XX Disclosure; Fig 3; 60pp; English.
XX

CC The invention relates to a novel method for preventing and/or inhibiting
CC cell death and/or tissue necrosis in a tissue comprising contacting the
CC live tissue with at least one segment of neural thread proteins (NTP).
CC The methods are composition are useful for treating a neurodegenerative
CC disorder, such as Alzheimer's disease. This sequence represents an NTP
CC protein of the invention
XX
SQ Sequence 112 AA;

Query Match 99.1%; Score 565; DB 6; Length 112;
Best Local Similarity 99.1%; Pred. No. 7.6e-57;
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLTSG 60
Db 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLTSG 60

Qy 61 DPPASAFQSAGITGVSHLTQPNLDKKKICSGNGSCYVAQAGLKLLASCNPSK 112
Db 61 DPPASAFQSAGITGVSHLTQPNLDKKKICSGNGSCYVAQAGLKLLASCNPSK 112

RESULT 8
ADB37521 standard; protein; 112 AA.
ID ADB37521 standard; protein; 112 AA.
XX
AC ADB37521;
XX
DT 04-DEC-2003 (first entry)
XX
DE Neural thread protein #2.
XX
KW Cytostatic; Antitumour; Antipsoriatic; Dermatological;
KW Antiatherosclerotic; Antiarteriosclerotic; Vasotropic; Antiinflammatory;
KW Immunosuppressive; Tranquillizer; Antiemetic; Virucide; AD7c-NTP;
KW neural thread protein; neuritic sprouting.
XX
OS Unidentified.
XX
XX WO2003008444-A2.
XX
XX 30-JAN-2003.
XX
XX 19-JUL-2002; 2002WO-CA001106.
XX
XX 19-JUL-2001; 2001US-0306150P.
XX
XX 19-JUL-2001; 2001US-0306161P.
XX
XX 16-NOV-2001; 2001US-0331477P.
XX
XX (NYMO-) NYMOX CORP.
XX
XX Averbach PA, Gemmell J;
XX
XX WPI; 2003-248000/24.
XX
XX Novel Related peptide or AD7c-neural thread peptide, useful for treating
XX unwanted cellular proliferations, glandular hyperplasia, unwanted facial
XX hair, warts and unwanted fatty tissue.
XX
XX Disclosure; Fig 3; 109pp; English.
XX
XX The present invention relates to AD7c-neural thread protein (NTP) and
XX related proteins and peptides (I; ADB37528-ADB37641). The sequences are
XX useful for treating a condition in a patient requiring removal or
XX destruction of cells. The condition can be selected from benign or
XX malignant tumour of a tissue, hyperplasia, hypertrophy or overgrowth of a
XX tissue, virally, bacterially or parasitically altered tissue, or
XX malformation of a tissue, where the tissue is selected from lung, breast,
XX stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney, sinus,
XX colon, intestine, stomach, rectum, oesophagus, heart, spleen, salivary
XX gland, blood, brain and its coverings, spinal cord and its coverings,
XX muscle, connective tissue, adrenal, parathyroid, thyroid, uterus, testis,
XX pituitary, reproductive organs, liver, gall bladder, eye, ear, nose,

CC throat, tonsils, mouth, lymph nodes and lymphoid tissue. The condition is
CC preferably tonsillar hypertrophy, prostatic hyperplasia, psoriasis,
CC eczema, dermatosis, cosmetic modification to a tissue (skin, eye, ear,
CC nose, throat, mouth, muscle, connective, hair or breast tissue), vascular
CC disease (atherosclerosis or arteriosclerosis), haemorrhoids, varicose
CC veins, inflammatory disease, autoimmune disease, metabolic injury,
CC hereditary/genetic disease, traumatic disease or physical injury,
CC nutritional deficiency disease, infectious disease, amyloid disease,
CC fibrosis disease, storage disease, congenital malformation, enzyme
CC deficiency disease, poisoning, intoxication, environmental disease,
CC radiation disease, endocrine disease, degenerative disease and mechanical
CC disease. The peptides are useful for treating unwanted cellular
CC proliferations, glandular (e.g. prostate) hyperplasia, unwanted facial
CC hair, warts and unwanted fatty tissue, or for preparing antibodies that
CC recognize and/or bind to Related proteins, Related peptides or NTP
XX peptides. The present sequence was used to illustrate the invention.
XX
SQ Sequence 112 AA;

Query Match 99.1%; Score 565; DB 7; Length 112;
Best Local Similarity 99.1%; Pred. No. 7.6e-57;
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLTSG 60
Db 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLTSG 60

Qy 61 DPPASAFQSAGITGVSHLTQPNLDKKKICSGNGSCYVAQAGLKLLASCNPSK 112
Db 61 DPPASAFQSAGITGVSHLTQPNLDKKKICSGNGSCYVAQAGLKLLASCNPSK 112

RESULT 9
ADC86487 standard; protein; 170 AA.
ID ADC86487 standard; protein; 170 AA.
XX
AC ADC86487;
XX
XX 01-JAN-2004 (first entry)
XX
XX Human GPCR protein SEQ ID NO:940.
XX
XX human; GPCR; guanosine triphosphate-binding protein coupled receptor;
XX gene therapy.
XX
XX Homo sapiens.
XX
XX EP1270724-A2.
XX
XX 02-JAN-2003.
XX
XX 18-JUN-2002; 2002EP-00013517.
XX
XX 18-JUN-2001; 2001JP-00246789.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
XX Suwa M, Asai K, Akiyama Y, Aburatani H;
XX
XX WPI; 2003-315783/31.
XX
XX N-PSDB; ADC86486.
XX
XX New polynucleotide, useful for preparing a composition for treating a
XX patient in need of increased or suppressed activity or expression of the
XX guanosine triphosphate-binding protein coupled receptor.
XX
XX Claim 2; SEQ ID NO 940; 28pp; English.
XX
XX The invention relates to a novel polynucleotide encoding a guanosine
XX triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
XX the invention may have a use in gene therapy. The polynucleotide and
XX polypeptide are useful for preparing a composition for treating a patient

CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The protein
CC sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
XX
SQ Sequence 170 AA;

Query Match 49.6%; Score 282.5; DB 7; Length 170;
Best Local Similarity 70.2%; Pred. No. 4.3e-24;
Matches 59; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

QY 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTP-LIFVFSLEAGFHHICQAGLKLLTS 59
Db 79 MVQSRLTATSASRVQAILLSQPPESLGLQVPATPSYFFIFLVETGFHCVGQAVLELLTS 138

QY 60 GDPASAFQSGAGITGVSHLTQAN 83
Db 139 GDPASASQSGAGISGVSHCARPLN 162

RESULT 10
ADC86543
ID ADC86543 standard; protein; 151 AA.
XX
AC ADC86543;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human GPCR protein SEQ ID NO:996.
XX
KW human; GPCR; guanosine triphosphate-binding protein coupled receptor;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN EP1270724-A2.
XX
PD 02-JAN-2003.
XX
PF 18-JUN-2002; 2002EP-00013517.
XX
PR 18-JUN-2001; 2001JP-00246789.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
PI Suwa M, Asai K, Akiyama Y, Aburatani H;
XX
XX
DR EP1270724-A2.
DR
PD 02-JAN-2003.
XX
PF 18-JUN-2002; 2002EP-00013517.
XX
PR 18-JUN-2001; 2001JP-00246789.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
PI Suwa M, Asai K, Akiyama Y, Aburatani H;
XX
XX
DR WPI; 2003-315783/31.
DR N-PSDB; ADC86542.
XX
PT New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.
XX
PS Claim 2; SEQ ID NO 996; 28pp; English.
XX
CC The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The protein
CC sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
XX
SQ Sequence 151 AA;

Query Match 44.1%; Score 251.5; DB 7; Length 151;
Best Local Similarity 67.9%; Pred. No. 1.4e-20;
Matches 55; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLLTSG 60
Db 57 VAQSRLTATSASRVQAILLPQPPEQLG-DMHHHTWLIFVFLVERGFHVGKAGLELLTSS 115

QY 61 DPPASAFQSGAGITGVSHLTQP 81
Db 116 DPPTSASQSGAGITGISHCARP 136

RESULT 11
ADC86547
ID ADC86547 standard; protein; 160 AA.
XX
AC ADC86547;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human GPCR protein SEQ ID NO:1000.
XX
KW human; GPCR; guanosine triphosphate-binding protein coupled receptor;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN EP1270724-A2.
XX
PD 02-JAN-2003.
XX
PF 18-JUN-2002; 2002EP-00013517.
XX
PR 18-JUN-2001; 2001JP-00246789.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
PI Suwa M, Asai K, Akiyama Y, Aburatani H;
XX
XX
DR WPI; 2003-315783/31.
DR N-PSDB; ADC86546.
XX
PT New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.
XX
PS Claim 2; SEQ ID NO 1000; 28pp; English.
XX
CC The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The protein
CC sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
XX
SQ Sequence 160 AA;

Query Match 42.1%; Score 240; DB 7; Length 160;
Best Local Similarity 63.9%; Pred. No. 3.1e-19;
Matches 53; Conservative 8; Mismatches 20; Indels 2; Gaps 1;

QY 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPA--NTPLIFVFSLEAGFHHICQAGLKLLT 58
Db 23 MVQSRLTATSASRVQAILLSQPPSELGLCTGACRHAQLIFCILMETGFHCVQAGLELLS 82

QY 59 SGDPASAFQSGAGITGVSHLTQP 81
Db 83 SGSPVVSASRSARITGVSHHWP 105

RESULT 12
ADR10295
ID ADR10295 standard; protein; 133 AA.
XX
AC ADR10295;
XX
DT 04-NOV-2004 (first entry)

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GenCore version 5.1.6
' Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:16 ; Search time 187.765 Seconds
(without alignments)
248.149 Million cell updates/sec

Title: US-10-092-934-3

Perfect score: 570

Sequence: 1 MAQSLTATSASRVOAILLS.....GSCVQAQGLKLLASCNPSK 112

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	570	100.0	112	14	US-10-138-516-2
2	570	100.0	112	14	US-10-146-130-4
3	570	100.0	112	14	US-10-092-934-3
4	570	100.0	112	14	US-10-153-334-3
5	570	100.0	112	14	US-10-198-069-3
6	570	100.0	112	14	US-10-198-070-3
7	570	100.0	112	14	US-10-294-891-2
8	570	100.0	112	17	US-10-920-313-2
9	282.5	49.6	170	14	US-10-017-161-1108
10	282.5	49.6	170	15	US-10-292-798-940
11	251.5	44.1	151	14	US-10-017-161-1178

12	251.5	44.1	151	15	US-10-292-798-996	Sequence 996, App
13	240	42.1	160	14	US-10-017-161-1184	Sequence 1184, App
14	240	42.1	160	15	US-10-292-798-1000	Sequence 1000, App
15	230.5	40.4	109	15	US-10-108-260A-2599	Sequence 2599, App
16	227.5	39.9	80	11	US-09-833-245-1403	Sequence 1403, App
17	227.5	39.9	80	11	US-09-833-245-1405	Sequence 1405, App
18	226.5	39.7	200	14	US-10-017-161-1242	Sequence 1242, App
19	226.5	39.7	200	15	US-10-292-798-1038	Sequence 1038, App
20	216	37.9	276	18	US-10-450-763-38278	Sequence 38278, App
21	214.5	37.6	123	14	US-10-198-070-44	Sequence 44, Appl
22	208	36.5	174	15	US-10-104-047-2183	Sequence 2183, App
23	204.5	35.9	116	11	US-09-989-890-206	Sequence 206, App
24	200	35.1	138	15	US-10-108-260A-3556	Sequence 3556, App
25	199	34.9	161	14	US-10-017-161-1730	Sequence 1730, App
26	199	34.9	161	15	US-10-292-798-1386	Sequence 1386, App
27	198.5	34.8	156	14	US-10-017-161-1850	Sequence 1850, App
28	198.5	34.8	156	15	US-10-292-798-1506	Sequence 1506, App
29	198	34.7	109	17	US-10-734-049A-274	Sequence 274, App
30	195.5	34.3	122	15	US-10-104-047-2490	Sequence 2490, App
31	195	34.2	113	15	US-10-104-047-2910	Sequence 2910, App
32	191	33.5	190	14	US-10-017-161-1734	Sequence 1734, App
33	191	33.5	190	15	US-10-292-798-1390	Sequence 1390, App
34	189	33.2	341	18	US-10-220-335-586	Sequence 586, App
35	188	33.0	127	14	US-10-074-475-215	Sequence 215, App
36	187	32.8	109	15	US-10-121-016-48	Sequence 48, Appl
37	182	31.9	143	10	US-09-974-879-533	Sequence 533, App
38	182	31.9	143	10	US-09-305-736-535	Sequence 535, App
39	182	31.9	143	10	US-09-818-683-535	Sequence 535, App
40	182	31.9	143	11	US-09-818-683-535	Sequence 533, App
41	182	31.9	143	15	US-10-621-401-533	Sequence 2377, App
42	181.5	31.8	129	10	US-09-764-891-2977	Sequence 2977, App
43	181.5	31.8	163	15	US-10-104-047-3081	Sequence 3081, App
44	181.5	31.8	603	16	US-10-408-765A-140	Sequence 140, App
45	180	31.6	155	14	US-10-017-161-1958	Sequence 1958, App

ALIGNMENTS

RESULT 1
US-10-138-516-2
; Sequence 2, Application US/10138516
; Publication No. US20030003445A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING ANTIBODIES TO
; TITLE OF INVENTION: NEURAL THREAD PROTEINS
; FILE REFERENCE: 59003.000004
; CURRENT APPLICATION NUMBER: US/10/138.516
; CURRENT FILING DATE: 2002-07-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-516-2

Query Match 100.0%; Score 570; DB 14; Length 112;
Best Local Similarity 100.0%; Pred. No. 5e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQSLTATSASRVOAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLTSG 60
Db 1 MAQSLTATSASRVOAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLTSG 60
Qy 61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNPSK 112
Db 61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNPSK 112

RESULT 2
US-10-146-130-4

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; Sequence 4, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; TITLE OF INVENTION: NEURAL THREAD PROTEINS
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-4

Query Match      100.0%; Score 570; DB 14; Length 112;
Best Local Similarity 100.0%; Pred. No. 5e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGPHHICQAGLKLLTSG 60
Db 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGPHHICQAGLKLLTSG 60

QY 61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNP SK 112
Db 61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNP SK 112

RESULT 3
US-10-092-934-3
; Sequence 3, Application US/10092934
; Publication No. US20030054990A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHODS OF USING NEURAL THREAD PROTEINS TO TREAT TUMORS
; TITLE OF INVENTION: AND CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018792-0199
; CURRENT APPLICATION NUMBER: US/10/092,934
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/273,957
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-934-3

Query Match      100.0%; Score 570; DB 14; Length 112;
Best Local Similarity 100.0%; Pred. No. 5e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGPHHICQAGLKLLTSG 60
Db 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGPHHICQAGLKLLTSG 60

QY 61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNP SK 112
Db 61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNP SK 112

RESULT 4
US-10-153-334-3
; Sequence 3, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
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; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003-000006
; CURRENT APPLICATION NUMBER: US/10/153,334
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,156
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-334-3

Query Match      100.0%; Score 570; DB 14; Length 112;
Best Local Similarity 100.0%; Pred. No. 5e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGPHHICQAGLKLLTSG 60
Db 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGPHHICQAGLKLLTSG 60

QY 61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNP SK 112
Db 61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNP SK 112

RESULT 5
US-10-198-069-3
; Sequence 3, Application US/10198069
; Publication No. US20030096756A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000009
; CURRENT APPLICATION NUMBER: US/10/198,069
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-069-3

Query Match      100.0%; Score 570; DB 14; Length 112;
Best Local Similarity 100.0%; Pred. No. 5e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGPHHICQAGLKLLTSG 60
Db 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGPHHICQAGLKLLTSG 60

QY 61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNP SK 112
Db 61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNP SK 112

RESULT 6
US-10-198-070-3
; Sequence 3, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMELL, JACK
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; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-070-3

Query Match      100.0%; Score 570; DB 14; Length 112;
Best Local Similarity 100.0%; Pred. No. 5e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60
Db      1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60

Qy      61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNPSK 112
Db      61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNPSK 112

RESULT 7
US-10-294-891-2
; Sequence 2, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-2

Query Match      100.0%; Score 570; DB 14; Length 112;
Best Local Similarity 100.0%; Pred. No. 5e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60
Db      1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60

Qy      61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNPSK 112
Db      61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNPSK 112

RESULT 8
US-10-920-313-2
; Sequence 2, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-2

Query Match      100.0%; Score 570; DB 14; Length 112;
Best Local Similarity 100.0%; Pred. No. 5e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60
Db      1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60

Qy      61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNPSK 112
Db      61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNPSK 112

RESULT 9
US-10-017-161-1108
; Sequence 1108, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: SUWA, MAKIKO
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1108
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-1108

Query Match      49.6%; Score 282.5; DB 14; Length 170;
Best Local Similarity 70.2%; Pred. No. 6.1e-24;
Matches 59; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

Qy      1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 59
Db      79 MVQSLRTATSASRVQAILLSQPPESLGLQVPATTPSYFFFLVETGFHCVGQAVLELLTS 138

Qy      60 GDPPASAFQSAGITGVSHLTQPAN 83
Db      139 GDPPASAFQSAGISGVSHCARPLN 162

RESULT 10
US-10-292-798-940
; Sequence 940, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
```

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; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-2

Query Match      100.0%; Score 570; DB 17; Length 112;
Best Local Similarity 100.0%; Pred. No. 5e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60
Db      1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60

Qy      61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNPSK 112
Db      61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNPSK 112

RESULT 9
US-10-017-161-1108
; Sequence 1108, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: SUWA, MAKIKO
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1108
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-1108

Query Match      49.6%; Score 282.5; DB 14; Length 170;
Best Local Similarity 70.2%; Pred. No. 6.1e-24;
Matches 59; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

Qy      1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 59
Db      79 MVQSLRTATSASRVQAILLSQPPESLGLQVPATTPSYFFFLVETGFHCVGQAVLELLTS 138

Qy      60 GDPPASAFQSAGITGVSHLTQPAN 83
Db      139 GDPPASAFQSAGISGVSHCARPLN 162

RESULT 10
US-10-292-798-940
; Sequence 940, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
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; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 940
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-940
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Query Match 49.6%; Score 282.5; DB 15; Length 170;
Best Local Similarity 70.2%; Pred. No. 6.1e-24;
Matches 59; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

QY 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTP-LIFVFSLEAGFHHICQAGLKLTSS 59
Db 79 MVQSRLTATSASRVQAILLPQPPEQLG-DMHHHTLWLFVFLVERGFHCVQAGLELLTS 138

QY 60 DPPASAFQSAGITGVSHLTQPN 83
Db 139 GDPPASASQAGISGVSHCARPLN 162
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RESULT 11
US-10-017-161-1178
; Sequence 1178, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1178
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-1178
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Query Match 44.1%; Score 251.5; DB 14; Length 151;
Best Local Similarity 67.9%; Pred. No. 1.8e-20;
Matches 55; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLTSG 60
Db 57 VAQSRLTATSASRVQAILLPQPPEQLG-DMHHHTLWLFVFLVERGFHCVQAGLELLTS 115

QY 61 DPPASAFQSAGITGVSHLTQPN 81
Db 116 DPPTSASQAGITGVSHCARP 136
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RESULT 12
US-10-292-798-996
; Sequence 996, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
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; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 996
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-996
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Query Match 44.1%; Score 251.5; DB 15; Length 151;
Best Local Similarity 67.9%; Pred. No. 1.8e-20;
Matches 55; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLTSG 60
Db 57 VAQSRLTATSASRVQAILLPQPPEQLG-DMHHHTLWLFVFLVERGFHCVQAGLELLTS 115

QY 61 DPPASAFQSAGITGVSHLTQPN 81
Db 116 DPPTSASQAGITGVSHCARP 136
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RESULT 13
US-10-017-161-1184
; Sequence 1184, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1184
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-1184
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Query Match 42.1%; Score 240; DB 14; Length 160;
Best Local Similarity 63.9%; Pred. No. 4.1e-19;
Matches 53; Conservative 8; Mismatches 20; Indels 2; Gaps 1;

QY 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPA--NTPLIFVFSLEAGFHHICQAGLKLT 58
Db 23 MVQSRLTATSASRVQAILLSQPPPELGLCTGACRHAQLIFCILMETGTGFHCVQAGLELLS 82

QY 59 SGDPASAFQSAGITGVSHLTQPN 81
Db 83 SGSPPVASASRSARITGVSHHAWP 105
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RESULT 14
US-10-292-798-1000
; Sequence 1000, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
```

; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1000
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-1000

Query Match 42.1%; Score 240; DB 15; Length 160;
Best Local Similarity 63.9%; Pred. No. 4.1e-19;
Matches 53; Conservative 8; Mismatches 20; Indels 2; Gaps 1;

Qy 1 MAQSLRTATSASRYQAILLSPKQLGLRAPA--NTPLIFVFSLEAGFHHCQAGLKLLT 58
Db 23 MVQSLRTATSTSRVQAILLSPPEELGLCTGACRHAQLIFCILMETGFHCVAQAAGLELLS 82

Qy 59 SGDPFPASAFQSAGITGVSHLTQP 81
Db 83 SGSPFVSASRSARITGVSHHAWP 105

RESULT 15
US-10-108-260A-2599
; Sequence 2599, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2599
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-2599

Query Match 40.4%; Score 230.5; DB 15; Length 109;
Best Local Similarity 66.7%; Pred. No. 3.1e-18;
Matches 54; Conservative 4; Mismatches 20; Indels 3; Gaps 1;

Qy 1 MAQSLRTATSASRYQAILLSPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60
Db 1 MAQSLWTATSVSQVQVILL---PKSGITGMHHHTRLIFVFLVEMGFHHIGQAGLELLTSG 57

Qy 61 DPPASAFQSAGITGVSHLTQP 81
Db 58 DPPASQSAGIAGVKHHAQP 78

Search completed: October 11, 2005, 07:39:43
Job time : 188.765 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:19 ; Search time 25.6043 Seconds
(without alignments)
326.535 Million cell updates/sec

Title: US-10-092-934-3
Perfect score: 570
Sequence: 1 MAQSRLTATSRSVQAILLS.....GSCVVAQAGLKLLASCNPSK 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	219	38.4	397	5	PCT-US95-17111A-121
2	215	37.7	92	4	US-09-621-976-5895
3	215	37.7	92	4	US-09-621-976-5901
4	215	37.7	92	4	US-09-621-976-5909
5	215	37.7	92	4	US-09-621-976-5914
6	182	31.9	74	4	US-09-513-999C-4478
7	176	30.9	74	4	US-09-513-999C-4488
8	174.5	30.6	99	4	US-09-288-143-168
9	167	29.3	144	4	US-09-513-999C-6953
10	165	28.9	90	3	US-09-227-357-171
11	164	28.8	90	4	US-09-513-999C-6012
12	163.5	28.7	108	4	US-09-513-999C-4433
13	161.5	28.3	239	4	US-09-800-729-193
14	161.5	28.3	310	4	US-09-800-729-190
15	161	28.2	112	4	US-09-513-999C-7870
16	160.5	28.2	95	4	US-09-621-976-5602
17	158	27.7	84	4	US-09-513-999C-4457
18	158	27.7	87	4	US-09-621-976-5672
19	157.5	27.6	85	4	US-09-513-999C-6550
20	156	27.4	88	4	US-09-621-976-5850
21	154	27.0	776	4	US-10-020-079-24
22	154	27.0	789	4	US-10-020-079-22
23	154	27.0	863	4	US-10-020-079-32
24	154	27.0	876	4	US-10-020-079-30
25	154	27.0	889	4	US-10-020-079-20
26	154	27.0	895	4	US-10-020-079-18
27	154	27.0	976	4	US-10-020-079-28

28	154	27.0	982	4	US-10-020-079-26	Sequence 26, Appl
29	152	26.7	72	4	US-09-513-999C-4419	Sequence 419, Ap
30	150.5	26.4	118	4	US-09-663-600A-114	Sequence 114, App
31	149.5	26.2	169	4	US-09-663-600A-208	Sequence 208, App
32	149	26.1	85	4	US-09-621-976-6679	Sequence 6679, Ap
33	149	26.1	94	4	US-09-621-976-4078	Sequence 4078, Ap
34	149	26.1	94	4	US-09-621-976-4079	Sequence 4079, Ap
35	148	26.0	71	4	US-09-621-976-5550	Sequence 5550, Ap
36	146	25.6	53	4	US-09-621-976-6507	Sequence 6507, Ap
37	143.5	25.2	70	4	US-09-621-976-4189	Sequence 4189, Ap
38	141	24.7	396	4	US-09-949-016-6783	Sequence 6783, Ap
39	141	24.7	442	4	US-09-949-016-6762	Sequence 762, Ap
40	140	24.6	53	4	US-09-513-999C-7092	Sequence 7092, Ap
41	138	24.2	52	4	US-09-513-999C-4441	Sequence 4441, Ap
42	137	24.0	52	4	US-09-513-999C-4444	Sequence 4444, Ap
43	137	24.0	96	4	US-09-513-999C-6065	Sequence 6065, Ap
44	136.5	23.9	638	4	US-09-949-016-11391	Sequence 11391, A
45	136	23.9	69	4	US-09-621-976-7243	Sequence 7243, Ap

ALIGNMENTS

RESULT 1
PCT-US95-17111A-121
; Sequence 121, Application PC/TUS9517111A
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
; TITLE OF INVENTION: Detection of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17111A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,426
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-17111A-121

Query Match 39.4%; Score 219; DB 5; Length 397;
Best Local Similarity 95.5%; Pred. No. 1.9e-18;
Matches 42; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 33 NTPLIFVFSLEAGPHHICQAGLKLLTSGDPPASAFQAGITGVTS 76
Db 349 HTPLIFVFSLEAGPHHICQAGLKLLTSGDPPASAFQAGITGVTS 392

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RESULT 2
US-09-621-976-5895
; Sequence 5895, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5895
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -46..-1
US-09-621-976-5895

Query Match      37.7%; Score 215; DB 4; Length 92;
Best Local Similarity 61.8%; Pred. No. 8.5e-19;
Matches 47; Conservative 4; Mismatches 25; Indels 0; Gaps 0;

QY 8 ATASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSGDPPASAF 67
   |||||:|||||
Db 2 ATFTSQVQVILLPQPLSSWDYRHAPTCPANFVFLVETGFLHVQAGLKLLTSGDPPASAS 61
   |||||:|||||

QY 68 QSAGITGVSHLTOPAN 83
   |||||:|||||
Db 62 QSAGITGVSHRAQPTS 77
   |||||:|||||

RESULT 3
US-09-621-976-5901
; Sequence 5901, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5901
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -46..-1
US-09-621-976-5901

Query Match      37.7%; Score 215; DB 4; Length 92;
Best Local Similarity 61.8%; Pred. No. 8.5e-19;
Matches 47; Conservative 4; Mismatches 25; Indels 0; Gaps 0;

QY 8 ATASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSGDPPASAF 67
   |||||:|||||
Db 2 ATFTSQVQVILLPQPLSSWDYRHAPTCPANFVFLVETGFLHVQAGLKLLTSGDPPASAS 61
   |||||:|||||

QY 68 QSAGITGVSHLTOPAN 83
   |||||:|||||
Db 62 QSAGITGVSHRAQPTS 77
   |||||:|||||

RESULT 4
US-09-621-976-5909
; Sequence 5909, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5909
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -46..-1
US-09-621-976-5909

Query Match      37.7%; Score 215; DB 4; Length 92;
Best Local Similarity 61.8%; Pred. No. 8.5e-19;
Matches 47; Conservative 4; Mismatches 25; Indels 0; Gaps 0;

QY 8 ATASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSGDPPASAF 67
   |||||:|||||
Db 2 ATFTSQVQVILLPQPLSSWDYRHAPTCPANFVFLVETGFLHVQAGLKLLTSGDPPASAS 61
   |||||:|||||

QY 68 QSAGITGVSHLTOPAN 83
   |||||:|||||
Db 62 QSAGITGVSHRAQPTS 77
   |||||:|||||

RESULT 5
US-09-621-976-5914
; Sequence 5914, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5914
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -46..-1
US-09-621-976-5914

Query Match      37.7%; Score 215; DB 4; Length 92;
Best Local Similarity 61.8%; Pred. No. 8.5e-19;
Matches 47; Conservative 4; Mismatches 25; Indels 0; Gaps 0;

QY 8 ATASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSGDPPASAF 67
   |||||:|||||
Db 2 ATFTSQVQVILLPQPLSSWDYRHAPTCPANFVFLVETGFLHVQAGLKLLTSGDPPASAS 61
   |||||:|||||

QY 68 QSAGITGVSHLTOPAN 83
   |||||:|||||
Db 62 QSAGITGVSHRAQPTS 77
   |||||:|||||
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Matches	34;	Conservative	4;	Mismatches	4;	Indels	0;	Gaps	0
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QY	36	LIFVFSLEAGFHHCQAGKLLTSGDPPASAFQSAGITGVSH	77
		: : : : :	
Db	9	LIFVLVTGFFHVGQAGLELTTSGDPPASASQAGITGLSH	50

RESULT 8

US-09-288-143-168

; Sequence 168, Application US/09288143

; Patent No. 6433139

; GENERAL INFORMATION:

; APPLICANT: Brewer et al.

; TITLE OF INVENTION: 53 Human Secreted Proteins

; FILE REFERENCE: P2018P1

; CURRENT APPLICATION NUMBER: US/09/288,143

; CURRENT FILING DATE: 1999-04-08

; EARLIER APPLICATION NUMBER: PCT/US98/21142

; EARLIER FILING DATE: 1998-10-08

; EARLIER APPLICATION NUMBER: 60/061,463

; EARLIER FILING DATE: 1997-10-09

; EARLIER APPLICATION NUMBER: 60/061,529

; EARLIER FILING DATE: 1997-10-09

; EARLIER APPLICATION NUMBER: 60/071,498

; EARLIER FILING DATE: 1997-10-09

; EARLIER APPLICATION NUMBER: 60/061,527

; EARLIER FILING DATE: 1997-10-09

; EARLIER APPLICATION NUMBER: 60/061,536

; EARLIER FILING DATE: 1997-10-09

; EARLIER APPLICATION NUMBER: 60/061,532

; EARLIER FILING DATE: 1997-10-09

; NUMBER OF SEQ ID NOS: 219

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 168

; LENGTH: 99

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-288-143-168

Query Match	30.6%;	Score	174.5;	DB	4;	Length	99;
Best Local Similarity	52.4%;	Pred. No.	8.8e-14;				
Matches	43;	Conservative	11;	Mismatches	27;	Indels	1;
Gaps							

QY	1	MAOSRLTATSASRVQAILLSQPPKQLGLRAPAN-TPLIFVPSLBAGFHHICQAGLKLLTS	59
		: : : : : : : : : : : : :	
Db	9	VVRSLWTATLASWVQAILMDSASQAGITSVHHQAQLSFVFLVEMLGLCHVQQAIGKLIIAS	68

QY	60	GDPPASAFQSAGITGVSHLTQP	81
		: : : :	
Db	69	SDFPASASQASAGITGMSSHWSWP	90

RESULT 9

US-09-513-999C-6953

; Sequence 6953, Application US/09513999C

; Patent No. 6783961

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; FILE REFERENCE: 59.US2.REG

; PATENT NO. 6783961

; CURRENT APPLICATION NUMBER: US/09/513,999C

; CURRENT FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 6953

; LENGTH: 144

; TYPE: PRT

; ORGANISM: Homo sapiens


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; LENGTH: 90
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6012

Query Match      28.8%; Score 164; DB 4; Length 90;
Best Local Similarity 64.6%; Pred. No. 1.5e-12;
Matches 31; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 33 NTPLIFFVFSLEAGFHHCQAGLKLLTSGDPPASAFQSGAGITGVSHLTQ 80
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 42 HTQLIFIFLVKTFPHVQGSHELLTSGDPPASASQASGAGITGMNHCAQ 89

RESULT 12
US-09-513-999C-4433
; Sequence 4433, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PATENT NO. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4433
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: -20...-1
; OTHER INFORMATION: score 8.4
; OTHER INFORMATION: seq FSLTVFLRQSFH/HV
US-09-513-999C-4433

Query Match      28.7%; Score 163.5; DB 4; Length 108;
Best Local Similarity 50.7%; Pred. No. 2.2e-12;
Matches 37; Conservative 7; Mismatches 16; Indels 13; Gaps 2;

Qy 21 QPP-----KQLGLRAPA-----NTPLIFVFSLEAGFHHCQAGLKLLTSGDPPASAF 67
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 36 QPPPRFKLLSCLSPQVGGITGTCHHAQLIFVFLIENGFFHVQAGLELLTSGDPPTSAS 95

Qy 68 QSGAGITGVSHLTQ 80
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 96 QPAGIIGMNHHAQ 108

RESULT 13
US-09-800-729-193
; Sequence 193, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 193
; LENGTH: 239

Query Match      28.3%; Score 161.5; DB 4; Length 310;
Best Local Similarity 54.7%; Pred. No. 1.6e-11;
Matches 35; Conservative 8; Mismatches 10; Indels 11; Gaps 1;

Qy 37 IFVFSLEAGFHHCQAGLKLLTSGDPPASAFQSGAGITGVSHLTOPANLDKKICNGGSCY 96
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 241 IFVFLVETGCHVQAGLELLISGDSPPASAFQSGAGITGVSHRARP-----GSVF 289

Qy 97 VAOA 100
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 290 LARS 293

RESULT 14
US-09-800-729-190
; Sequence 190, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 190
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-190

Query Match      28.3%; Score 161.5; DB 4; Length 310;
Best Local Similarity 54.7%; Pred. No. 1.6e-11;
Matches 35; Conservative 8; Mismatches 10; Indels 11; Gaps 1;

Qy 37 IFVFSLEAGFHHCQAGLKLLTSGDPPASAFQSGAGITGVSHLTOPANLDKKICNGGSCY 96
   |||:|:|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|
Db 241 IFVFLVETGCHVQAGLELLISGDSPPASAFQSGAGITGVSHRARP-----GSVF 289

Qy 97 VAOA 100
   :|:|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|
Db 290 LARS 293

RESULT 15
US-09-513-999C-7870
; Sequence 7870, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PATENT NO. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7870
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -49...-1
; OTHER INFORMATION: score 7.7
; OTHER INFORMATION: seq LCLLGSSDSPASA/SQ
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 55
; OTHER INFORMATION: Xaa=Ser or Thr
US-09-513-999C-7870

Query Match      28.2%; Score 161; DB 4; Length 112;
Best Local Similarity 69.2%; Pred. No. 4.7e-12;
Matches 36; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

Qy 33 NTPLIIFVFSLEAGFHHICQAGLKLLTSGDPPASAFOSAGITGVSHLTQPNL 84
Db 61 HTQLIFVFLIETGFLHIGQAALLETSGDPPASASOSAGITGVX--TTPGRL 110

Search completed: October 11, 2005, 07:42:47
Job time : 26.6043 secs
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QY 5 KSSLVL-----LLCLTCSYAFMFSSLRQK-----TSE-PQGVKPCGEHFRIRQNL 48
Db 74 KSQLIQRHGHTGKPTCTECGSGFRHKQVLMRHFQIHTGCKEYECTQCGEGFLLSKL 133
QY 49 PEHTQGLGSKWLWLLFAVVPFVILKCORDSEKNKVRMAPFFLH 92
Db 134 IHORGHGTGK-----PFMTECGKGFQRQKVLIHQFIH 168

RESULT 3
I48689
gene NK10 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48689; S49078
R;Lange, R.; Christoph, A.; Thiesen, H.J.; Vopper, G.; Johnson, K.R.; Lemaire, L.; Plom
DNA Cell Biol. 14, 971-981, 1995
A;Title: Developmentally regulated mouse gene NK10 encodes a xZinc Finger Repressor Prot
A;Reference number: I48689; MUID:9609544; PMID:7576184
A;Accession: I48689
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-636 <RES>
A;Cross-references: UNIPROT:Q61967; EMBL:X79828; NID:g506501; PIDN:CAA56225.1; PID:g5065
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match 13.5%; Score 77.5; DB 2; Length 636;
Best Local Similarity 29.9%; Pred. No. 0.95;
Matches 26; Conservative 8; Mismatches 34; Indels 19; Gaps 4;

QY 13 CLTCSYAF-MFSSLRQKTS-PQGVK-----CGEHFRIRQNLPEHTQGLGSKWLWLLFA 66
Db 552 CIDCGKAFSSSLIQHTHTGKPKYECNCGRAFRKTNLDHQRTHGTGK----- 604
QY 67 VVPFVILKCORDSEKNKVRMAPFFLH 93
Db 605 --PYACEGCR---NFSRSSALTKHH 625

RESULT 4
C31201
GLI-related finger protein HKR1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: C31201
R;Ruppert, J.M.; Kinzler, K.W.; Wong, A.J.; Bigner, S.H.; Kao, F.T.; Law, M.L.; Seunaez,
Mol. Cell. Biol. 8, 3104-3113, 1988
A;Title: The GLI-Kruppel family of human genes.
A;Reference number: A93103; MUID:89096896; PMID:2850480
A;Accession: C31201
A;Molecule type: DNA
A;Residues: 1-224 <RUP>
A;Cross-references: UNIPROT:P10072
C;Keywords: DNA binding; zinc finger

Query Match 12.8%; Score 73.5; DB 2; Length 224;
Best Local Similarity 30.0%; Pred. No. 0.94;
Matches 21; Conservative 6; Mismatches 28; Indels 15; Gaps 3;

QY 12 LCLTCSYAF-----MFSSLRQKTS-PQGVKPCGEHFRIRQNLPEHTQGLGSKWLWLLF 65
Db 139 ICRECEQGSQKGLIRHLRHTHTGKPYVTECGRHFWSKNLKTQRTHSQVK----- 192
QY 66 AVVPFVILKC 75
Db 193 ---PYVCLEC 199

RESULT 5
S75655
anhranilate synthase (EC 4.1.3.27) component I - Synecchocystis sp. (strain PCC 6803)
N;Alternate names: protein slr1979
C;Species: Synecchocystis sp.
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75655
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shampo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75655
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-485 <KAN>
A;Cross-references: UNIPROT:P74130; EMBL:D90912; GB:AB001339; NID:G1653228; PIDN:BAA18211
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: trpE
A;Start codon: GTG
C;Superfamily: anhranilate synthase component I
C;Keywords: carbon-carbon lyase; oxo-acid-lyase

Query Match 12.8%; Score 73.5; DB 2; Length 485;
Best Local Similarity 26.1%; Pred. No. 2;
Matches 36; Conservative 9; Mismatches 36; Indels 57; Gaps 8;

QY 1 MWTLKSSVLLCLTCSYAFMFSSLRQKTS-PQGVKPCGEHFRIRQNLPEHTQ-----G 54
Db 95 LWTPKPEEI-----FSFLNQ-----LCPCNHDVNLTKNIPHELPHGGLG 135
QY 55 WLGSKWLW-----LJFAVV-----PFVILKQCR-----DSEKNKVRMAP 88
Db 136 WLGYDTAWAIEKLUPYSKADLDLPPVAYWYEPENFVILDHQLLWLTATTQDEKIK----- 190
QY 89 FELHHI-DSISGVSGKRM 105
Db 191 FFOQLADKINSVSPQV 208

RESULT 6
T21225
hypothetical protein F21H7.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21225
R;Gardner, A.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z19393
A;Accession: T21225
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-569 <WIL>
A;Cross-references: UNIPROT:O9XTV8; EMBL:Z93379; PIDN:CAB07593.1; GSPDB:GN00023; CESP:F21
C;Genetics:
A;Experimental source: clone F21H7
A;Gene: CESP:F21H7.7
A;Map position: 5
A;Introns: 122/1; 344/2; 455/1; 539/1

Query Match 12.5%; Score 71.5; DB 2; Length 569;
Best Local Similarity 28.6%; Pred. No. 4;
Matches 18; Conservative 14; Mismatches 12; Indels 19; Gaps 4;

QY 12 LCLTCSYAFMFSSLRQKTS-PQGVKPCGEHFRIRQNLPEHTQGLGSKWLWLLFAVVPF 70
Db 121 ICAICSYTYLFES--RSSSLPQNR-----FRISRRKI-----KFLYFFVFLPFP 162
QY 71 VIL 73
Db 163 ILI 165

RESULT 7
S47067
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 63.6283 Seconds
(without alignments)
853.085 Million cell updates/sec

Title: US-10-092-934-4
Perfect score: 573
Sequence: 1 MWTLKSSLVLLCLTCSYAF.....APFLHHIDSISGVSGKMP 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	426	74.3	94	2 Q9HCV7	Q9hc77 homo sapien
2	283	49.4	138	2 Q9HCV6	Q9hc66 homo sapien
3	258.5	45.1	170	2 Q9D9T2	Q9d9t2 mus musculus
4	84.5	14.7	653	2 Q64RH7	Q64rh7 bacteroides
5	81	14.1	380	2 Q83C2	Q83c2 mus musculus
6	81	14.1	435	1 Z022.XENLA	P18745 xenopus lae
7	81	14.1	463	2 Q8ZPG0	Q8zpg0 mus musculus
8	81	14.1	530	2 Q8F9Y7	Q8f9y7 mus musculus
9	80	14.0	276	2 Q9NPP0	Q9np00 homo sapien
10	80	14.0	545	2 Q86XJ3	Q86xj3 homo sapien
11	79.5	13.9	196	1 ZG64.XENLA	P18732 xenopus lae
12	77.5	13.5	636	1 ZF90.MOUSE	Q61967 mus musculus
13	77	13.4	140	2 Q8C194	Q8c194 mus musculus
14	77	13.4	330	2 Q95L04	Q95l04 macaca fasc
15	77	13.4	487	2 Q8TF53	Q8tf53 homo sapien
16	77	13.4	532	2 Q8N141	Q8n141 homo sapien
17	77	13.4	532	2 Q8NC63	Q8nc63 homo sapien
18	76	13.3	300	2 Q8CRL6	Q8crl6 mus musculus
19	76	13.3	813	2 Q8P1W5	Q8piw5 mus musculus
20	76	13.3	832	2 Q8BUQ3	Q8buq3 mus musculus
21	74.5	13.0	310	2 Q8DJZ0	Q8djz0 homo sapien
22	74.5	13.0	366	2 Q6ZML3	Q6zml3 homo sapien
23	74.5	13.0	382	2 Q6DD87	Q6dd87 homo sapien
24	74.5	13.0	385	2 Q00455	Q00455 homo sapien
25	74.5	13.0	478	2 Q6R2H7	Q6r2h7 human echov
26	74.5	13.0	537	2 Q6NSZ9	Q6nsz9 homo sapien
27	74.5	13.0	683	1 Z263.HUMAN	O14978 homo sapien
28	74	12.9	305	2 Q7SEU8	Q7seu8 neurospora
29	74	12.9	317	2 Q8TA07	Q8ta07 homo sapien
30	73.5	12.8	485	1 TRE2.SYNY3	P74130 synechocyst
31	73.5	12.8	598	2 Q7Z6E1	Q7z6e1 homo sapien

ALIGNMENTS

RESULT 1

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Q9HCV7 ID Q9HCV7 PRELIMINARY; PRT; 94 AA.
AC Q9HCV7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DJ1153D9.3 (Novel protein).
GN Name=DJ1153D9.3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Clark G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL109806; CAC03742.1;
SQ SEQUENCE 94 AA; 11060 MW; E0AB7D817888A06C CRC64;
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Query Match 74.3%; Score 426; DB 2; Length 94;
Best Local Similarity 95.2%; Pred. No. 1.9e-39;
Matches 79; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 MWTLKSSLVLLCLTCSYAFMFSSLRKTSPOQKVPQGEHFRIRQNLPEHTQGLGSKW 60
Db 1 MWTLKSSLVLLCLTCSYAFMFSSLRKTSPOQKVPQGEHFRIRQNLPEHTQGLGSKW 60
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Qy 61 LWLLFAVVVPFVILKCORDSEKNK 83
Db 61 LWLLFAVVVPFVILKCORDSEKNK 83
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RESULT 2

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AC Q9HCV6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE DJ1153D9.4 (Novel protein) (Fragment).
GN Name=DJ1153D9.4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Clark G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL109806; CAC03743.1;
DR Genew; HGNC:16101; C20orf107.
FT NON TER
SQ SEQUENCE 138 AA; 15703 MW; E2D80F4A92B464BF CRC64;
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AC	P18745;
DT	01-NOV-1990 (Rel. 16, Created)
DT	01-NOV-1990 (Rel. 16, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Oocyte zinc finger protein XLCOF22
OS	Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC	Xenopodinae; Xenopus.
OX	NCBI_TaxID=8355;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=8905062; PubMed=3139407;
RA	Koester M., Pieler T., Poeting A., Knoechel W.;
RT	"The finger motif defines a multigene family represented in the
RL	mammalian mRNA of Xenopus laevis oocytes.";
RT	EMBO J. 7:1735-1741(1988).
DR	PIR; S00833; S00833.
DR	HSP; P08047; ISP2.
DR	InterPro; IPR007087; Znf_C2H2.
DR	InterPro; IPR007086; Znf_C2H2_sub.
DR	Pfam; PF00096; zf-C2H2_12.
DR	PRINTS; PR00048; ZINCFINGER.
DR	ProDom; PD000003; Znf_C2H2; 12.
DR	SMART; SM00355; Znf_C2H2; 12.
DR	PROSITE; PS00028; ZINC_FINGER_C2H2_1; 12.
DR	PROSITE; PS0157; ZINC_FINGER_C2H2_2; 12.
KW	DNA-binding; Metal-binding; Repeat; Zinc-finger.
FT	ZN FING 97 120
FT	ZN_FING 126 148
FT	ZN_FING 153 176
FT	ZN_FING 154 176
FT	ZN_FING 182 204
FT	ZN_FING 210 232
FT	ZN_FING 238 260
FT	ZN_FING 266 288
FT	ZN_FING 294 316
FT	ZN_FING 322 345
FT	ZN_FING 351 373
FT	ZN_FING 379 402
FT	ZN_FING 408 430
SQ	SEQUENCE 435 AA; 49416 MW; FE83299ACFD4D8F3 CRC64;
Query Match 14.1%; Score 81; DB 1; Length 435;	
Best Local Similarity 26.1%; Pred. No. 1.9;	
Matches 24; Conservative 12; Mismatches 32; Indels 24; Gaps 4	
Qy	13 CLTCSYAFMFSSL---RQKT---SEPGKVP CGEHFRIRQNLPHTQGWLGSKWLLWLFPA 66 : : : : : : : : : : :
Db	184 CLECGCKFLFRSLRHQRTHTGKPPFSCLCKGKCFSVRSRLKDHRHTTGK----- 236 : : : : : : : : : : :
Qy	67 VVPEVLKQCR-----DSEKNKYRMAPP 89 : : : : : : : : : : :
Db	237 --PFSCLEGCKSFSPRECLIDHQRTHTGKERPF 266 : : : : : : : : : : :
RESULT 7	
Q6ZPGO	
ID	Q6ZPGO PRELIMINARY; PRT; 463 AA.
AC	Q6ZPGO;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	MKIAA1948 protein (Fragment).
GN	Name=mKIAA1948;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	Tissue=Embryonic tail;
RX	PubMed=14621295;

RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129467; BAC98277.1; -.
DR HSSP; P03001; 1UN6.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 13.
DR ProDom; PD000003; Znf_C2H2; 13.
DR SMART; SM00355; Znf_C2H2; 13.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 12.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 13.
FT NON_TER 1
SQ SEQUENCE 463 AA; 54252 MW; 2043BD957A8F277CE CRC64;
Query Match 14.1%; Score 81; DB 2; Length 463;
Best Local Similarity 29.0%; Pred. No. 2;
Matches 27; Conservative 10; Mismatches 36; Indels 20; Gaps 4;
QY 13 CLTCSYAF-MFSSLRQKTSBPQKVP-----CGEHFRIRQLNPEHTQGWLGSKWLLPFA 66
DB 355 CKDCGAFRLLSQLTQHSVHAGEKPYSCKECKSFRLQKLAHQSIHTGK----- 407
QY 67 VVPFVLKCORDSEKNKVRMAPFLHHIDSIG 99
DB 408 --PFECKECKR-----AFRLNSSLIQHLRIHSG 433
RESULT 8
Q6P9Y7
ID Q6P9Y7 PRELIMINARY; PRT; 530 AA.
AC Q6P9Y7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schner A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RC

RA Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC060530; AAH60530.1; -.
DR HSSP; P03001; 1UN6.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001909; KRAB.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF01352; KRAB; 1.
DR ProDom; PD00096; zf-C2H2; 13.
DR SMART; SM00349; KRAB; 1.
DR SMART; SM00355; Znf_C2H2; 13.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 12.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 13.
KW Hypothetical protein.
SQ SEQUENCE 530 AA; 62122 MW; 87CFAFB2A3CF1BD6 CRC64;
Query Match 14.1%; Score 81; DB 2; Length 530;
Best Local Similarity 29.0%; Pred. No. 2.3;
Matches 27; Conservative 10; Mismatches 36; Indels 20; Gaps 4;
QY 13 CLTCSYAF-MFSSLRQKTSBPQKVP-----CGEHFRIRQLNPEHTQGWLGSKWLLPFA 66
DB 422 CKDCGAFRLLSQLTQHSVHAGEKPYSCKECKSFRLQKLAHQSIHTGK----- 474
QY 67 VVPFVLKCORDSEKNKVRMAPFLHHIDSIG 99
DB 475 --PFECKECKR-----AFRLNSSLIQHLRIHSG 500
RESULT 9
Q9NPP0
ID Q9NPP0 PRELIMINARY; PRT; 276 AA.
AC Q9NPP0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Auffray C., Ansoerge W., Ballabio A., Estivill X., Gibson K.,
RA Lehrach H., Poustka A., Lundeberg J.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Carim L., Estivill X., Escarceller M., Sumoy L.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL365370; CAB96946.1; -.
DR HSSP; P25490; 1UBD
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR007087; Znf_C2H2.
DR InterPro; IPR007086; Znf_C2H2_sub.
DR Pfam; PF00096; zf-C2H2; 9.
DR PRINTS; PR00048; ZINC_FINGER.
DR ProDom; PD000003; Znf_C2H2; 10.
DR SMART; SM00355; Znf_C2H2; 10.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 10.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 10.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 276 AA; 31538 MW; 8EB93052A59B8E4E CRC64;
Query Match 14.0%; Score 80; DB 2; Length 276;
RC

[illegible]

```
RESULT 12
ZF90 MOUSE
ID_ZF90_MOUSE STANDARD; PRT; 636 AA.
AC Q61967;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Zinc finger protein 90 (Zfp-90) (Zinc finger protein NK10).
GN Name=zf90; Synonyms=NK10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=96069544; PubMed=7576184;
RA Lange R., Christoph A., Thiesen H.-J., Vopper G., Johnson K.R.,
RA Lemaire L., Plomann M., Cremer H., Barthele D., Heinlein U.A.O.;
RT "Developmentally regulated mouse gene NK10 encodes a zinc finger
RT repressor protein with differential DNA-binding domains.";
RL DNA Cell Biol. 14:971-981(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N-3; TISSUE=Mammary gland;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May function as a repressor or silencer protein, and
CC most likely exerts its repressing activity upon zinc-dependent
CC binding to DNA. May be involved in proper spermatogenesis by
CC repressing the expression of genes unnecessary or incompatible
CC with the maintenance of a haploid cell state.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Brain, heart, spleen, thymus, and testis.
CC -!- DEVELOPMENTAL STAGE: There is a marked increase after postnatal
CC stages 18-20 (simultaneously to the appearance of haploid cell
CC stages). Maximal expression is observed around 2 weeks
CC postnatally, with the exception of brain and testis, where the
CC expression is highest in earlier developmental stages.
CC -!- SIMILARITY: Belongs to the krueppel C2H2-type zinc-finger protein
CC family.
CC -!- SIMILARITY: Contains 13 C2H2-type zinc fingers.
CC -!- SIMILARITY: Contains 1 KRAB domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X79828; CAA56225.1; -.
DR EMBL; BC046298; AAH46298.1; -.
PIR; I48689; I48689.
HSSP; P08047; ISP2.
MGD; MGI:104786; Zfp90.
InterPro; IPR001909; KRAB.
InterPro; IPR007087; Znf_C2H2.
InterPro; IPR007086; Znf_C2H2_sub.
Pfam; PF01352; KRAB; 1.
Pfam; PF00096; zf-C2H2; 13.
PRINTS; PD00048; ZINCFINGER.
PROSITE; PS00003; Znf_C2H2; 10.
PROSITE; PS08005; KRAB; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 13.
PROSITE; PS00157; ZINC_FINGER_C2H2_2; 13.
KW DNA-binding; Metal-binding; Nuclear protein; Repeat; Repressor;
KW Transcription regulation; Zinc-finger.
FT DOMAIN 14 85
FT ZN_FING 208 230 C2H2-type 1.
FT ZN_FING 250 272 C2H2-type 2.
FT ZN_FING 278 300 C2H2-type 3.
FT ZN_FING 306 328 C2H2-type 4.
FT ZN_FING 334 356 C2H2-type 5.
FT ZN_FING 362 384 C2H2-type 6.
FT ZN_FING 390 412 C2H2-type 7.
FT ZN_FING 446 468 C2H2-type 8.
FT ZN_FING 494 516 C2H2-type 9.
FT ZN_FING 522 544 C2H2-type 10.
FT ZN_FING 550 572 C2H2-type 11.
FT ZN_FING 578 600 C2H2-type 12.
FT ZN_FING 606 628 C2H2-type 13.
SQ SEQUENCE 636 AA; 72423 MW; 1269BEC7729E369F CRC64;
Query Match 13.5%; Score 77.5; DB 1; Length 636;
Best Local Similarity 29.9%; Pred. No. 6.9;
Matches 26; Conservative
QY 13 CUTCSVAF-MFSSLROKTSPOQKVP-----CGEHFRIRQNLPEHTQGWLGSKWMLLFA 66
Db 552 CIDCGKAFSSQSSLIQHERTHTGKPYECNECGRAFRRKTKNLHDHQRTHGTEK----- 604
QY 67 VVPFVLKQDSEKKNKVRMAPFFLHH 93
Db 605 --PYACKCEGR----NFSRSALTQKH 625
RESULT 13
R8CL194 PRELIMINARY; PRT; 140 AA.
ID Q8C194;
AC Q8C194;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:4732438E01 product:MOB1 PROTEIN (HYPOTHETICAL 25.1 kDa
DE PROTEIN) homolog.
GN Name=Mobk1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
```

Hypothetical protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecidae; Macaca.
NCBI_TaxID=9541;
[1]
SEQUENCE FROM N.A.
TISSUE=Testis;
RA Osada N., Hida M., Kusuda J., Tanuma R., Hirata M., Suto Y., Hirai M.,
Terao K., Sugano S., Hashimoto K.;
"Cynomolgus monkey testicular cDNAs for discovery of novel human genes
in the human genome sequence.";
BMC Genomics 3:36-36(2002).
EMBL; AB071098; BAB64492.1; -.
HSSP; P25490; 1UBD.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001909; KRAB.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF01352; KRAB; 1.
DR Pfam; PF00096; zf-C2H2; 6.
DR ProDom; PD000003; Znf_C2H2; 6.
DR SMART; SM00349; KRAB; 1.
DR SMART; SM00355; Znf_C2H2; 6.
DR PROSITE; PS08005; KRAB; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 6.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 6.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 330 AA; 39099 MW; 44E0A040AE999BB CRC64;

Query Match 13.4%; Score 77; DB 2; Length 330;
Best Local Similarity 29.0%; Pred. No. 4;
Matches 27; Conservative 10; Mismatches 36; Indels 20; Gaps 4;

QY 13 CLTCSYAF-MFSSLRQKTSEPOGKVP-----CGEHFPIRQNLPEHTOGWLGSKWLWLLFA 66
Db 222 CXECGKAFRLLSLTQHQSITHCEKPKYKCECKGKAPRLQKLTILHQSIHTGEEK----- 274

QY 67 VVPFVLKQDSEKKNKVRMAPFFLHHDSIG 99
Db 275 --PFPECKEGRK-----AFRLNSSLIQHLRIHSG 300

RESULT 15
Q8TF53 PRELIMINARY; PRT; 487 AA.
ID Q8TF53 AC Q8TF53;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE KIAA1948 protein (fragment).
Name=KIAA1948;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21842142; PubMed=11853319;
RA Nagase T., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XXII.
RT The complete sequences of 50 new cDNA clones which code for large
RT proteins.";
RL DNA Res. 8:319-327(2001).
RL EMBL; AB075828; BAB85534.1; -.
DR HSSP; P08046; IF2I.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.

```
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 13.
DR ProDom; PD000003; Znf_C2H2; 13.
DR SMART; SM00355; Znf_C2H2; 13.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 12.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 13.
FT NON_TER 1
SQ SEQUENCE 487 AA; 57086 MW; F529A5495FC9E136 CRC64;

Query Match      13.4%; Score 77; DB 2; Length 487;
Best Local Similarity 29.0%; Pred. No. 6;
Matches 27; Conservative 10; Mismatches 36; Indels 20; Gaps 4;

Qy      13 CLTCSYAF-MFSSLRQKTSBPQKVP-----CGEHFRIRQNLPEHTQGLGSKWLWLLFA 66
Db      379 CKECGKAFRLLSQLTQHSIHGKPKYKCKEKGKAFRLRQKLTILHQSIHTGK-----431

Qy      67 VVPFVILKQDSEKKNVRMAPFLHHIDSIG 99
Db      432 --PFECKECKR-----AFRLNSSLIOHLRIHSG 457
```

Search completed: October 11, 2005, 07:18:45
Job time : 66.6283 secs

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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 78.508 Seconds
(without alignments)
522.196 Million cell updates/sec

Title: US-10-092-934-4
Perfect score: 573
Sequence: 1 MWTLKSLVLLCLTCSYAF.....APFLHHIDISGVSGKRMF 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_l6Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	100.0	106	5 AAE29145	Aae29145 Neural th
2	573	100.0	106	6 ABR63243	Abf63243 106 amino
3	573	100.0	106	6 ABU02975	Abu02975 Human neu
4	573	100.0	106	6 ABP59926	Abp59926 Human 106
5	573	100.0	106	6 AAE33192	Aae33192 Neural th
6	573	100.0	106	6 ABJ19448	Abj19448 106-mer n
7	573	100.0	106	7 ADB37522	Adb37522 Neural th
8	573	100.0	106	7 ADL96024	Adl96024 Human neu
9	453	79.1	171	6 ABU12055	Abu12055 Human NOV
10	430	75.0	171	3 AAY53032	Aay53032 Human sec
11	430	75.0	239	6 AAU68550	Aau68550 Human nov
12	430	75.0	239	6 ABR58389	Abf58389 Human NOV
13	430	75.0	292	8 ADS10718	Adf10718 Human the
14	423	73.8	101	2 AAY12683	Aay12683 Human 5'
15	423	73.8	101	3 AAG00463	Aag00463 Human sec
16	358	62.5	156	6 ABU12061	Abu12061 Human NOV
17	358	62.5	156	6 ABU12060	Abu12060 Human NOV
18	358	62.5	156	6 ABU12058	Abu12058 Human NOV
19	354	61.8	156	6 ABU12059	Abu12059 Human NOV
20	339	59.2	156	6 ABU12062	Abu12062 Human NOV
21	252	44.0	47	6 ABU12056	Abu12056 Human NOV
22	233	40.7	47	6 ABU12057	Abu12057 Human NOV
23	92	16.1	15	6 ABP59901	Abp59901 Human neu
24	92	16.1	15	7 ADL96047	Adl96047 Human neu
25	87	15.2	15	6 ABP59900	Abp59900 Human neu

26	87	15.2	15	7 ADL96046	Adl96046 Human neu
27	83	14.5	16	6 ABP59904	Abp59904 Human neu
28	83	14.5	16	7 ADL96050	Adl96050 Human neu
29	80	14.0	15	6 ABP59902	Abp59902 Human neu
30	80	14.0	15	7 ADL96048	Adl96048 Human neu
31	80	14.0	513	4 AAB73600	Aab73600 Zinc fing
32	80	14.0	545	8 ADM87387	Adm87387 Human pro
33	78.5	13.7	111	8 ADP70944	Adp70944 Novel zin
34	78.5	13.7	111	8 ADP70943	Adp70943 Novel zin
35	78	13.6	15	6 ABP59903	Abp59903 Human neu
36	78	13.6	15	7 ADL96049	Adl96049 Human neu
37	77	13.4	15	6 ABP59899	Abp59899 Human neu
38	77	13.4	15	7 ADL96045	Adl96045 Human neu
39	77	13.4	194	7 ADL22738	Adl22738 Human dis
40	77	13.4	424	6 ABU11725	Abu11725 Human MDD
41	77	13.4	429	5 ABB98780	Abb98780 Human mac
42	77	13.4	475	8 ABM82090	Abm82090 Tumour-as
43	77	13.4	532	4 AAM93834	Aam93834 Human pol
44	77	13.4	532	8 ADL31870	Adl31870 Human pro
45	76	13.3	15	6 ABP59898	Abp59898 Human neu

ALIGNMENTS

RESULT 1
AAE29145
ID AAE29145 standard; protein; 106 AA.
XX
AC AAE29145;
XX
DT 27-JAN-2003 (first entry)
XX
DE Neural thread protein (NTP) #3.

Neural thread protein; NTP; hyperplasia; hypertrophy; arteriosclerosis; haemorrhoid; gene therapy; tumour; vascular disease; atherosclerosis; inflammatory disease; nutritional deficiency disease; genetic disease; autoimmune disease; metabolic disease; traumatic disease; intoxication; infectious disease; congenital malformation; enzyme deficiency disease; amyloid disease; fibrosis disease; storage disease; radiation disease; poisoning; environmental disease; endocrine disease; protein therapy; degenerative disease; mechanical disease.

Unidentified.

WO200274323-A2.

26-SEP-2002.

08-MAR-2002; 2002WO-IB001959.

08-MAR-2001; 2001US-0273957P.

(AVER/) AVERAGE P.

Average P;

WPI; 2002-759864/82.

Treating a condition in a patient requiring removal or destruction of cells, such as a benign or malignant tumor of a tissue or an inflammatory disease, comprises administering a neural thread protein (NTP) or a NTP gene to a mammal.

Claim 23; Fig 4; 70pp; English.

The invention relates to a method for treating a condition in a patient requiring removal or destruction of cells. The method involves administering to a mammal a neural thread protein (NTP), or administering to a tumour or other target cell a NTP gene, where the expression of the NTP gene is induced resulting in expression of the NTP protein. The method and NTP are useful for treating a condition in a patient requiring

CC removal or destruction of cells, such as a benign or malignant tumour of
CC a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue,
CC preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,
CC bacterially, or parasitically altered tissue, or a malformation of a
CC tissue. Other conditions include a cosmetic modification to a tissue,
CC such as removal of unwanted facial hair, warts or unwanted fatty tissue,
CC a vascular disease, particularly atherosclerosis or arteriosclerosis,
CC haemorrhoids, or varicose veins, an inflammatory disease, autoimmune
CC disease, metabolic disease, hereditary/genetic disease, traumatic disease
CC or physical injury, nutritional deficiency disease, infectious disease,
CC congenital malformation, amyloid disease, fibrosis disease, storage
CC disease, enzyme deficiency disease, poisoning, intoxication, degenerative
CC disease, radiation disease, environmental disease, endocrine disease or
CC mechanical disease. The invention is useful in protein therapy and gene
CC therapy. The present sequence is NTP protein
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 573; DB 5; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1e-64;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWTLKSSLVLLCLCTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
Db 1 MWTLKSSLVLLCLCTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
Qy 61 LLLFAVVPFVILKQDSEKKNVRMAPFFLHHIDSISGVSGKRMF 106
Db 61 LLLFAVVPFVILKQDSEKKNVRMAPFFLHHIDSISGVSGKRMF 106

RESULT 2
ABR63243
ID ABR63243 standard; protein; 106 AA.
AC ABR63243;
XX
XX
XX
DT 28-AUG-2003 (first entry)
DE 106 amino acid neural thread protein.
XX
XX
KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour.
XX
OS Unidentified.
XX
PN WO2003008443-A2.
XX
PD 30-JAN-2003.
XX
XX 19-JUL-2002; 2002WO-CA001105.
XX
PR 19-JUL-2001; 2001US-0306150P.
PR 19-JUL-2001; 2001US-0306161P.
PR 16-NOV-2001; 2001US-0331477P.
XX
XX (NYMO-) NYMOX CORP.
XX
XX Averbach PA;
XX
XX WPI; 2003-247999/24.
XX

Novel neural thread protein peptide, referred as cell death peptide,
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
XX
PS Disclosure; Fig 4; 77pp; English.
XX
XX The present invention relates to a neural thread protein (NTP) peptide
CC referred to as cell death peptide. Thought to be cytostatic,
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC treating a condition in a patient requiring removal or destruction of
CC cells, for treating a condition such as benign or malignant tumor,
XX

CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for
CC a pancreatic thread protein. The peptide is conjugated, linked or bound
CC to a molecule chosen from antibody or its fragment, antibody-like binding
CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side
CC effects of surgery. The present sequence is an NTP amino acid sequence
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 573; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1e-64;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWTLKSSLVLLCLCTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
Db 1 MWTLKSSLVLLCLCTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
Qy 61 LLLFAVVPFVILKQDSEKKNVRMAPFFLHHIDSISGVSGKRMF 106
Db 61 LLLFAVVPFVILKQDSEKKNVRMAPFFLHHIDSISGVSGKRMF 106

RESULT 3
ABU02975
ID ABU02975 standard; protein; 106 AA.
AC ABU02975;
XX
XX
DT 20-JAN-2003 (first entry)
DE Human neural thread protein AD7C-NTP, protein fragment #3.
XX
XX
KW Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;
KW transplantation; grafting; chemotherapy; immunotherapy; vaccination;
KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;
KW radiation; tumour; hyperplasia; hypertrophy; overgrowth of tissue;
KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;
KW cosmetic modification; vascular disease; atherosclerosis;
KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;
KW autoimmune disease; metabolic disease; traumatic disease;
KW physical injury; nutritional deficiency disease; infectious disease;
KW amyloid disease; fibrosis disease; storage disease;
KW congenital malformation; enzyme deficiency disease; poisoning;
KW intoxication; environmental disease; radiation disease;
KW endocrine disease; degenerative disease; mechanical disease.
XX
OS Homo sapiens.
XX
XX WO200297030-A2.
XX
XX 05-DEC-2002.
XX
XX 24-MAY-2002; 2002WO-CA000759.
XX
XX 25-MAY-2001; 2001US-0293156P.
XX
XX (NYMO-) NYMOX CORP.
XX
XX Averbach PA;
XX
XX WPI; 2003-041406/03.
XX

Novel peptides similar in amino acid sequence to neural thread proteins
PT (NTP), useful for treating unwanted cellular proliferations such as
PT malignant tumors and prostatic hyperplasia.
XX
XX Disclosure; Fig 4; 78pp; English.
XX
XX The invention describes an NTP-peptide (I) comprising at least one amino
CC acid sequence corresponding to part of the amino acid sequence of a
CC neural thread protein, AD7C-NTP. The invention provides a method of

CC treating a condition requiring removal or destruction of cells of a
 CC mammal comprising administering to a mammal, a therapeutic amount of (I).
 CC The treatment is administered to the mammal before, during or after
 CC surgical excision, transplantation, grafting, chemotherapy,
 CC immunotherapy, vaccination, thermal or electrical ablation,
 CC laser therapy, phototherapy, gene therapy and/or radiation. The method is
 CC useful for treatment of benign or malignant tumour; hyperplasia,
 CC hyperthyroidism or overgrowth of tissue; virally, bacterially or
 CC parasitically altered tissue; malformation of tissue selected from lung,
 CC breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,
 CC sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary
 CC gland, blood, brain and its coverings, spinal cord, muscle, connective
 CC tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary,
 CC reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,
 CC tonsils, mouth and lymph nodes and lymphoid system; tonsillary
 CC hyperthyroidism; prostatic hyperplasia; cosmetic modification to a tissue;
 CC vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;
 CC varicose veins; inflammatory disease; autoimmune disease; metabolic
 CC disease; hereditary/genetic disease; traumatic disease; physical injury;
 CC nutritional deficiency disease; infectious disease; amyloid disease;
 CC fibrosis disease; storage disease; congenital malformation; enzyme
 CC deficiency disease; poisoning; intoxication; environmental disease;
 CC radiation disease; endocrine disease; degenerative disease and mechanical
 CC disease. This is the amino acid sequence of a human neural thread protein
 CC AD7C-NTP protein fragment
 CC
 CC SQ Sequence 106 AA;

Query Match 100.0%; Score 573; DB 6; Length 106;
 Best Local Similarity 100.0%; Pred. No. 1.1e-64;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWTLKSSLVLLCLTCSYAFMFSSLRKTSPPQKVPCEGHEFRIRQNLPEHTQGLGSKW 60
 Db 1 MWTLKSSLVLLCLTCSYAFMFSSLRKTSPPQKVPCEGHEFRIRQNLPEHTQGLGSKW 60
 Qy 61 LWWLFAVVPFVILKQDSEKKNVMAFFLHHIDISGVSGKRMF 106
 Db 61 LWWLFAVVPFVILKQDSEKKNVMAFFLHHIDISGVSGKRMF 106

RESULT 4

ABP59926
 ID ABP59926 standard; protein; 106 AA.

AC ABP59926;

DT 08-SEP-2003 (first entry)

DE Human 106 amino acid neural thread protein-like protein.

XX Human; tumour; cancer; neural thread protein; NTP; cell removal;
 KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;
 KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;
 KW gene therapy.

XX Homo sapiens.

XX WO2003044053-A2.

XX 30-MAY-2003.

XX 18-NOV-2002; 2002WO-CA001757.

XX 16-NOV-2001; 2001US-0331477P.

XX (NYMO-) NYMOX CORP.

XX Averbach P, Gemmell J;

XX WPI; 2003-457592/43.

PT New neural thread protein (NTP), useful for preparing a composition for

PT treating or preventing a condition in a mammal requiring removal or
 PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or
 PT inflammatory disease.

XX Disclosure; Fig 3; 98pp; English.

XX The present invention relates to peptides derived from the human neural
 CC thread protein (NTP). The peptides are useful for preparing a composition
 CC for treating or preventing a condition in a mammal requiring removal or
 CC destruction of cells, comprising tonsillary hypertrophy, prostatic
 CC hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a
 CC breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,
 CC varicose veins, atherosclerosis, inflammatory, metabolic, infectious,
 CC fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,
 CC occlusion or blockage of an artery or of a stent placed or implanted in
 CC an artery. The present sequence is an NTP protein used to produce
 CC peptides of the invention

XX SQ Sequence 106 AA;

Query Match 100.0%; Score 573; DB 6; Length 106;
 Best Local Similarity 100.0%; Pred. No. 1.1e-64;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWTLKSSLVLLCLTCSYAFMFSSLRKTSPPQKVPCEGHEFRIRQNLPEHTQGLGSKW 60
 Db 1 MWTLKSSLVLLCLTCSYAFMFSSLRKTSPPQKVPCEGHEFRIRQNLPEHTQGLGSKW 60
 Qy 61 LWWLFAVVPFVILKQDSEKKNVMAFFLHHIDISGVSGKRMF 106
 Db 61 LWWLFAVVPFVILKQDSEKKNVMAFFLHHIDISGVSGKRMF 106

RESULT 5

AAE33192
 ID AAE33192 standard; protein; 106 AA.

XX AAE33192;

XX 16-APR-2003 (first entry)

XX Neural thread protein (NTP) #3.

XX Cell death; tissue necrosis; neural thread protein; NTP; amyloidosis;
 KW stroke; brain tumour; Pick's disease; Parkinson's disease; glaucoma;
 KW Alzheimer's disease; gene therapy.

XX Unidentified.

XX WO200289841-A2.

XX 14-NOV-2002.

XX 06-MAY-2002; 2002WO-CA000681.

XX 04-MAY-2001; 2001US-0288463P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-120506/11.

XX Preventing, controlling, modulating, ameliorating and/or treating cell
 PT death or tissue necrosis using antibodies to neural thread proteins,
 PT useful in disorders such as stroke, brain tumor, glaucoma and Alzheimer's
 PT disease.

XX Disclosure; Fig 7; 60pp; English.

XX The invention relates to a method of preventing, and/or inhibiting cell
 CC death and/or tissue necrosis in live tissue containing neural thread
 CC proteins (NTP). The method involves contacting the live tissue with at

CC least one antibody, fragment or derivative that recognises NTP, where the
CC antibody, fragment or derivative is present to prevent, control,
CC ameliorate and/or inhibit cell death and/or tissue necrosis caused by the
CC presence of NTP. Methods and compositions of the invention are useful for
CC preventing, modulating, controlling and/or treating disorders associated
CC with cell death and/or tissue necrosis such as stroke, brain tumour,
CC Pick's disease, Parkinson's disease, amyloidosis, glaucoma and
CC Alzheimer's disease. The invention is useful in gene therapy. The present
CC sequence is NTP protein
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 573; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1e-64;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWTLKSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
Db |||||
1 MWTLKSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
QY 61 LWLLFAVVPFVILKQDSEKKNVRMAPFFLHHIDISISGVSGKRMF 106
Db |||||
61 LWLLFAVVPFVILKQDSEKKNVRMAPFFLHHIDISISGVSGKRMF 106

RESULT 6
ABJ19448
ID ABJ19448 standard; protein; 106 AA.
XX
AC ABJ19448;
DT 27-MAR-2003 (first entry)
XX
DE 106-mer neural thread protein #1.
XX
XX Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.
XX
OS Unidentified.
XX
XX WO200292115-A2.
XX
XX 21-NOV-2002.

XX
XX 16-MAY-2002; 2002WO-CA000712.
XX
XX 16-MAY-2001; 2001US-0290971P.
XX
XX (NYMO-) NYMOX CORP.
XX
XX Averbach PA;
XX
XX WPI; 2003-129234/12.
XX
XX Preventing and/or inhibiting cell death and/or tissue necrosis in a
PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
PT disease, by contacting the live tissue with at least one segment of
PT neural thread proteins (NTP).
XX
XX Disclosure; Fig 4; 60pp; English.

XX The invention relates to a novel method for preventing and/or inhibiting
CC cell death and/or tissue necrosis in a tissue comprising contacting the
CC live tissue with at least one segment of neural thread proteins (NTP).
CC The methods are composition are useful for treating a neurodegenerative
CC disorder, such as Alzheimer's disease. This sequence represents an NTP
CC protein of the invention
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 573; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1e-64;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWTLKSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
Db |||||
1 MWTLKSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
QY 61 LWLLFAVVPFVILKQDSEKKNVRMAPFFLHHIDISISGVSGKRMF 106
Db |||||
61 LWLLFAVVPFVILKQDSEKKNVRMAPFFLHHIDISISGVSGKRMF 106

RESULT 7
ADB37522
ID ADB37522 standard; protein; 106 AA.
XX
AC ADB37522;
XX
DT 04-DEC-2003 (first entry)
XX
DE Neural thread protein-like protein #1.
XX
KW Cytostatic; Antitumour; Antipsoriatic; Dermatological;
KW Antiatherosclerotic; Antiarteriosclerotic; Vasotropic; Antiinflammatory;
KW Immunosuppressive; Tranquillizer; Antileptic; Virucide; AD7c-NTP;
KW neural thread protein; neuritic sprouting.
XX
OS Unidentified.
XX
XX WO2003008444-A2.
XX
XX 30-JAN-2003.
XX
XX 19-JUL-2002; 2002WO-CA001106.
XX
XX 19-JUL-2001; 2001US-0306150P.
PR 19-JUL-2001; 2001US-0306161P.
PR 16-NOV-2001; 2001US-0331477P.
XX
XX (NYMO-) NYMOX CORP.
XX
XX Averbach PA, Gemmell J;
PI
XX WPI; 2003-248000/24.
XX
XX Novel Related peptide or AD7c-neural thread peptide, useful for treating
PT unwanted cellular proliferations, glandular hyperplasia, unwanted facial
PT hair, warts and unwanted fatty tissue.
XX
XX Disclosure; Fig 4; 109pp; English.

XX The present invention relates to AD7c-neural thread protein (NTP) and
CC related proteins and peptides (I; ADB37528-ADB37641). The sequences are
CC useful for treating a condition in a patient requiring removal or
CC destruction of cells. The condition can be selected from benign or
CC malignant tumour of a tissue, hyperplasia, hypertrophy or overgrowth of a
CC tissue, virally, bacterially or parasitically altered tissue, or
CC malformation of a tissue, where the tissue is selected from lung, breast,
CC stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney, sinus,
CC colon, intestine, stomach, rectum, oesophagus, heart, spleen, salivary
CC gland, blood, brain and its coverings, spinal cord and its coverings,
CC muscle, connective tissue, adrenal, parathyroid, thyroid, uterus, testis,
CC pituitary, reproductive organs, liver, gall bladder, eye, ear, nose,
CC throat, tonsils, mouth, lymph nodes and lymphoid tissue. The condition is
CC preferably tonsillar hypertrophy, prostatic hyperplasia, psoriasis,
CC eczema, dermatosis, cosmetic modification to a tissue (skin, eye, ear,
CC nose, throat, mouth, muscle, connective, hair or breast tissue), vascular
CC disease (atherosclerosis or arteriosclerosis), haemorrhoids, varicose
CC veins, inflammatory disease, autoimmune disease, metabolic disease,
CC hereditary/genetic disease, traumatic disease or physical injury,
CC nutritional deficiency disease, infectious disease, amyloid disease,
CC fibrosis disease, storage disease, congenital malformation, enzyme
CC deficiency disease, poisoning, intoxication, environmental disease,
CC radiation disease, endocrine disease, degenerative disease and mechanical
CC disease. The peptides are useful for treating unwanted cellular

CC proliferations, glandular (e.g. prostate) hyperplasia, unwanted facial
CC hair, warts and unwanted fatty tissue, or for preparing antibodies that
CC recognize and/or bind to related proteins, Related peptides or NTP
CC peptides. The present sequence was used to illustrate the invention.

XX SQ Sequence 106 AA;

Query Match 100.0%; Score 573; DB 7; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1e-64;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSBPQGVPCGEHFRIRQNLPEHTQGLGSKW 60

Db 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSBPQGVPCGEHFRIRQNLPEHTQGLGSKW 60

Oy 61 LWLLFAVVPFVILKQDSEKNKVRMAPFFLHHIDSISGVSGKRMF 106

Db 61 LWLLFAVVPFVILKQDSEKNKVRMAPFFLHHIDSISGVSGKRMF 106

RESULT 8
ADL96024
ID ADL96024 standard; protein; 106 AA.

XX AC ADL96024;

DT 20-MAY-2004 (first entry)

XX DE Human neural thread protein, NTP106.

XX KW Human; neural thread protein; NTP122; NTP112; NTP106; NTP98; NTP75;
KW NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;
KW eczema; haemorrhoid; atherosclerosis; inflammatory disease;
KW autoimmune disease; metabolic disease; hereditary disease;
KW genetic disease; traumatic disease; physical injury;
KW nutritional deficiency disease; infectious disease; amyloid disease;
KW Alzheimer's disease; storage disease; congenital malformation;
KW enzyme deficiency disease; poisoning; intoxication;
KW environmental disease; radiation disease; endocrine disease;
KW degenerative disease; mechanical disease.

XX OS Homo sapiens.

XX PN US2003166569-A1.

XX PD 04-SEP-2003.

XX PF 15-NOV-2002; 2002US-00294891.

XX PR 16-NOV-2001; 2001US-0331477P.

XX PA (AVER/) AVERBACK P.

XX PA (GEMM/) GEMMELL J.

XX PI Averbach P, Gemmell J;

XX DR WPI; 2003-898099/82.

XX PT New neural thread protein or its variants, useful for treating tumors and
XX other conditions requiring the removal or destruction of cells (e.g.
XX prostatic hyperplasia, psoriasis, eczema, hemorrhoids or
XX atherosclerosis).

XX PS Disclosure; SEQ ID NO 3; 32pp; English.

XX CC The invention relates to a peptide, or its homologue, derivative,
XX fragment, variant or mimetic, comprising at least one neural thread
XX protein (NTP) peptide appearing as ADL96029-ADL96069, derived from
XX NTP122, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid
XX encoding an amino acid sequence corresponding to the above peptide, a
XX composition comprising one or more peptides or nucleic acids cited above
XX and a carrier, a method of treating a condition in a mammal requiring
XX removal or destruction of cells (comprising administering to the mammal

CC an amount of the peptide cited above) and a method of preventing or
CC inhibiting the stenosis, occlusion or blockage of a stent, comprising
CC coating the stent with an amount of the above peptide. The peptide
CC further comprises an amino acid in a reverse-D order based on the above
CC amino acid sequences. The composition and methods are useful in treating
CC tumours and other conditions requiring the removal or destruction of
CC cells (e.g. prostatic hyperplasia, psoriasis, eczema, hemorrhoids or
CC atherosclerosis). These may also be used in treating inflammatory
CC diseases, autoimmune diseases, metabolic diseases, hereditary/genetic
CC diseases, traumatic diseases or physical injuries, nutritional deficiency
CC diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,
CC storage diseases, congenital malformation, enzyme deficiency diseases,
CC poisoning, intoxication, environmental diseases, radiation diseases,
CC endocrine diseases, degenerative diseases or mechanical diseases. The
CC present sequence is a human NTP protein from which the peptides of the
XX invention are derived.

XX SQ Sequence 106 AA;

Query Match 100.0%; Score 573; DB 7; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1e-64;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSBPQGVPCGEHFRIRQNLPEHTQGLGSKW 60

Db 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSBPQGVPCGEHFRIRQNLPEHTQGLGSKW 60

Oy 61 LWLLFAVVPFVILKQDSEKNKVRMAPFFLHHIDSISGVSGKRMF 106

Db 61 LWLLFAVVPFVILKQDSEKNKVRMAPFFLHHIDSISGVSGKRMF 106

RESULT 9

ABU12055

ID ABU12055 standard; protein; 171 AA.

XX AC ABU12055;

XX DT 19-FEB-2003 (first entry)

XX DE Human NOV10a CG90739-01 protein SEQ ID 30.

XX KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
KW antilipaeamic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
KW metabolic syndrome X; wasting disease.

XX OS Homo sapiens.

XX PN WO200281625-A2.

XX PD 17-OCT-2002.

XX PF 03-APR-2002; 2002WO-US010366.

XX PR 03-APR-2001; 2001US-0281086P.

XX PR 05-APR-2001; 2001US-0281906P.

XX PR 06-APR-2001; 2001US-0282020P.

XX PR 10-APR-2001; 2001US-0282930P.

XX PR 12-APR-2001; 2001US-0283444P.

XX PR 13-APR-2001; 2001US-0283512P.

XX PR 13-APR-2001; 2001US-0283657P.

XX PR 13-APR-2001; 2001US-0283710P.

XX PR 17-APR-2001; 2001US-0284234P.

XX PR 19-APR-2001; 2001US-0285325P.

XX PR 20-APR-2001; 2001US-0285381P.

XX PR 24-APR-2001; 2001US-0286068P.

XX PR 25-APR-2001; 2001US-0286292P.

XX PR 07-JUN-2001; 2001US-0296692P.

RESULT 11
AAU68550
ID AAU68550 standard; protein: 239 AA.
AC AAU68550;
DT 16-JAN-2002 (first entry)
XX Human novel cytokine encoded by cDNA 790CIP2D_11 #1.
DE Human; cytokine; cell proliferation; cell differentiation;
KW anti-inflammatory; stem cell growth factor; activin; inhibin; cancer;
KW nervous system disease; neuropathy; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; spinal cord disorder;
KW head trauma; stroke; myeloid cell disorder; lymphoid cell disorder;
KW platelet disorder; thrombocytopaenia; stem cell disorder;
KW aplastic anaemia; tissue regeneration; wound healing; ulcer;
KW osteoporosis; osteoarthritis; bone degenerative disorder;
KW periodontal disease; fibrosis; reperfusion; immune disorder; SCID;
KW severe combined immunodeficiency; infection; autoimmune disorder;
KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; allergy;
KW asthma; coagulation disorder; haemophilia; sepsis; nephritis;
KW inflammatory bowel disease; food supplement; immunogen.
XX Homo sapiens.
OS
XX
XX WO200175093-A1.
PN
XX
XX 11-OCT-2001.
PD
XX
XX 30-MAR-2001; 2001WO-US010484.
FF
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
PR 22-SEP-2000; 2000US-00668680.
PR 23-OCT-2000; 2000US-00895618.
PR 30-NOV-2000; 2000US-00728711.
PR 14-MAR-2001; 2001US-00808701.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
PI Xu C, Yang Y, Zaho QA, Chen R, Wang D, Goodrich RW, Liu C;
PI Drmanac RT;
XX
XX WPI: 2001-626432/72.
DR N-PSDB; AAS59642.
DR
XX
XX New polypeptides and nucleic acids, useful for diagnosis, treatment of
PT inflammatory, autoimmune, neurological, myeloid or lymphoid cell, bone
PT degenerative disorders, cancer and promoting wound healing.
XX
XX Claim 20; Page 274; 336pp; English.
PS
XX
XX The invention relates to isolated human polypeptides (which may be
CC cytokines) and the polynucleotides encoding them. The protein is useful
CC for identifying a compound which binds to it (e.g. modulators, agonists
CC and antagonists). The polynucleotides are useful as an array for mismatch
CC detection. The proteins and nucleic acids are useful as nutritional
CC sources or supplements. The protein exhibits activity relating
CC to cytokine, cell proliferation, cell differentiation, anti-inflammatory,
CC stem cell growth factor activity, immune stimulating or immune
CC suppressing and activin or inhibin related activities. The proteins (and
CC antibodies raised against them) and nucleic acids are therefore useful in
CC the diagnosis and treatment of diseases and disorders such as cancer,
CC central and peripheral nervous system diseases and neuropathies,
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, spinal cord disorders, head trauma, cerebrovascular
CC diseases, stroke, myeloid or lymphoid cell disorders, platelet disorders,
CC thrombocytopaenia, stem cell disorders, aplastic anaemia, for
CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
CC growth, and in tissue repair, healing of burns, incisions, ulcers, for
CC treating osteoporosis, osteoarthritis, bone degenerative disorders, or

CC periodontal disease, lung or liver fibrosis, reperfusion injury in
CC various tissues, various immune deficiencies and disorders including
CC severe combined immunodeficiency (SCID), bacterial or fungal infections,
CC autoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis,
CC diabetes mellitus, myaesthesia gravis), allergic reactions and conditions,
CC such as asthma or other respiratory problems, coagulation disorders,
CC haemophilia), septic shock, sepsis, arthritis, nephritis and inflammatory
CC bowel disease, viral infection and are useful in altering bodily
CC characteristics. The present sequence represents a novel protein of the
CC invention
XX
SQ Sequence 239 AA;
Query Match 75.0%; Score 430; DB 4; Length 239;
Best Local Similarity 90.9%; Pred. No. 5.2e-46;
Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 1 MWTLKSLVLLCLTCSYAFMFSSLRKTSBPQKVGCFHFRIRQLPEHTQGLGSKW 60
Db 69 MWTLKSLVLLCLTCSYAFMFSSLRKTSBPQKVGCFHFRIRQLPEHTQGLGSKW 128
Qy 61 LWLLFAVVVPFVILKCORDSEKNKVRMAP 88
Db 129 LWLLFAVVVPFVILKCORDSEKNKVSPP 156
RESULT 12
ABR58389
ID ABR58389 standard; protein: 239 AA.
XX
AC ABR58389;
XX
DT 07-JUL-2003 (first entry)
XX Human NOV13a.
XX
KW Human; NOV; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective; dyslipidaemia;
KW antiparkinsonian; antilipaeamic; gene therapy; metabolic disorder;
KW diabetes; obesity; infection; cachexia; cancer; Parkinson's disease;
KW neurodegenerative disorder; Alzheimer's disease; immune disorder;
KW haematopoietic disorder.
XX
XX Homo sapiens.
XX
XX WO2003029423-A2.
PN
XX
PD 10-APR-2003.
XX
XX 02-OCT-2002; 2002WO-US031358.
PF
XX
XX 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327342P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 12-APR-2002; 2002US-0371972P.
PR 12-APR-2002; 2002US-0371980P.
PR 17-APR-2002; 2002US-0373261P.
PR 19-APR-2002; 2002US-0373805P.
PR 23-APR-2002; 2002US-0374738P.
PR 16-MAY-2002; 2002US-0381101P.
PR 17-MAY-2002; 2002US-0381635P.
PR 29-MAY-2002; 2002US-0383830P.

```

PR 01-OCT-2002; 2002US-00262839.
XX (CURA-) CURAGEN CORP.
PA
XX
XX Alsbrook JP, Anderson DW, Boldog FL, Burgess CE, Catterton E;
PI Edinger SR, Ellerman K, Gerlach VL, Gorman L, Guo X, Ji W;
PI Kekuda R, Leach MD, Li L, Miller CE, Patturajan M, Rieger DK;
PI Rothenberg MB, Shimkets RA, Smithson G, Spytek KA, Taupier RJ;
PI Vernet CAM, Voss EZ, Zethusen BD, Zhong M;
XX
DR WPI; 2003-381625/36.
DR N-PSDB; ACC72103.
XX
XX NOVX polypeptides and nucleic acids useful for diagnosing or
PT treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or
PT dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 146; 487pp; English.
XX
XX The present invention relates to novel human NOV proteins and their
CC coding sequences (ACC72075-ACC72181 and ABR58363-ABR58469). The NOV
CC proteins are useful in manufacturing a medicament for treating a syndrome
CC associated with a human disease. The NOV proteins and coding sequences
CC may be used to diagnose, treat or prevent metabolic disorders such as
CC diabetes or obesity, infections, cachexia, cancer, neurodegenerative
CC disorders such as Alzheimer's disease or Parkinson's disease, immune
CC disorders, haematopoietic disorders and various dyslipidaemias
XX
XX Sequence 239 AA;
SQ
Query Match 75.0%; Score 430; DB 6; Length 239;
Best Local Similarity 90.9%; Pred. No. 5.2e-46;
Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 MWTLKSSLVLLCLCTCSYAFMFSSLRQKTSEPOGKVP CGEHFRIQNLPEHTQGLGSKW 60
Db 69 MWTLKSSLVLLCLCTCSYAFMFSSLRQKTSEPOGKVP CGEHFRIQNLPEHTQGLGSKW 128
QY 61 LWLLFAVVPFVILKQDSEKKNVMAP 88
Db 129 LWLLFVVVPFVILQCRDSEKKNQSP 156
RESULT 13
ADSL0718
ID ADSL0718 standard; protein; 292 AA.
XX
XX ADSL0718;
XX
XX 16-DEC-2004 (first entry)
XX
XX Human therapeutic protein - SEQ ID 955.
XX
XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;
XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
XX aplastic anaemia; cancer; wound healing, gene therapy.
XX
XX Homo sapiens.
XX
XX WO2004080148-A2.
XX
XX 23-SEP-2004.
XX
XX 30-SEP-2003; 2003WO-US030720.
XX
XX 02-OCT-2002; 2002US-0416186P.
XX
XX (NUVE-) NUVELO INC.
XX
XX Tang YT, Asundi V, Ren F, Zhang J, Zhang J, Wehrman T, Wang Z, Ma Y;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX

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DR WPI; 2004-668857/65.
DR N-PSDB; ADS10034.
XX
XX New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.
XX
XX Claim 20; SEQ ID NO 955; 718pp; English.
XX
XX The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic protein
CC of the invention. The current sequence is not shown explicitly within the
XX CC specification but can be accessed from the WIPO web-site.
SQ Sequence 292 AA;
Query Match 75.0%; Score 430; DB 8; Length 292;
Best Local Similarity 90.9%; Pred. No. 6.6e-46;
Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 MWTLKSSLVLLCLCTCSYAFMFSSLRQKTSEPOGKVP CGEHFRIQNLPEHTQGLGSKW 60
Db 122 MWTLKSSLVLLCLCTCSYAFMFSSLRQKTSEPOGKVP CGEHFRIQNLPEHTQGLGSKW 181
QY 61 LWLLFAVVPFVILKQDSEKKNVMAP 88
Db 182 LWLLFVVVPFVILQCRDSEKKNQSP 209
RESULT 14
AAV12683
ID AAV12683 standard; protein; 101 AA.
XX
XX AAV12683;
XX
XX 21-JUN-1999 (first entry)
XX
XX Human 5' EST secreted protein SEQ ID NO:273.
XX
XX Human; secreted protein; EST; expressed sequence tag; diagnosis;
XX forensic; gene therapy; chromosome mapping; signal peptide;
XX upstream regulatory sequence; cytokine activity; cell proliferation;
XX differentiation; haematopoiesis regulation; tissue growth regulation;
XX reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
XX thrombolytic; anti-inflammatory; tumour inhibition.
XX
XX Homo sapiens.
XX
XX WO9906549-A2.
XX
XX 11-FEB-1999.
XX
XX 31-JUL-1998; 98WO-IB001231.
XX
XX 01-AUG-1997; 97US-00905279.
XX
XX (GEST ) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Lacroix B;
PI
XX WPI; 1999-153779/13.
DR N-PSDB; AAX51461.
XX
XX New nucleic acids encoding human secreted proteins - obtained from cDNA
PT libraries derived from testis, ovary, uterus and spleen tissue.
XX
XX Claim 34; Page 384; 522pp; English.
PS

```



```
CC AAX51459 to AAX51691 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins, and encode the proteins given in AAY12681 to
CC AAY12913, respectively. The proteins given represent the signal peptide
CC and an N-terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell
XX
SQ Sequence 101 AA;

Query Match 73.8%; Score 423; DB 2; Length 101;
Best Local Similarity 89.8%; Pred. No. 1.4e-45;
Matches 79; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MWTLKSSILVLLCLTCSYAFMFSSLRQKTSPPQKVPCEHFRIRQNLPEHTQGLGSKW 60
Db 1 MWTLKSSILVLLCLTCSYAFMFSSLRQKTSPPQKVPCEHFRIRQNLPEHTQGLGSKW 60

Qy 61 LWLLFAVVVPFVILKCORDSEKKNKVRMAP 88
Db 61 LWLLXVVVPFVILQCRDSEKKNKQSP 88

Search completed: October 11, 2005, 07:11:04
Job time : 80.508 secs

CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors
XX
SQ Sequence 101 AA;

Query Match 73.8%; Score 423; DB 3; Length 101;
Best Local Similarity 89.8%; Pred. No. 1.4e-45;
Matches 79; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MWTLKSSILVLLCLTCSYAFMFSSLRQKTSPPQKVPCEHFRIRQNLPEHTQGLGSKW 60
Db 1 MWTLKSSILVLLCLTCSYAFMFSSLRQKTSPPQKVPCEHFRIRQNLPEHTQGLGSKW 60

Qy 61 LWLLFAVVVPFVILKCORDSEKKNKVRMAP 88
Db 61 LWLLXVVVPFVILQCRDSEKKNKQSP 88

Search completed: October 11, 2005, 07:11:04
Job time : 80.508 secs

CC AAX51459 to AAX51691 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins, and encode the proteins given in AAY12681 to
CC AAY12913, respectively. The proteins given represent the signal peptide
CC and an N-terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell
XX
SQ Sequence 101 AA;

Query Match 73.8%; Score 423; DB 2; Length 101;
Best Local Similarity 89.8%; Pred. No. 1.4e-45;
Matches 79; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MWTLKSSILVLLCLTCSYAFMFSSLRQKTSPPQKVPCEHFRIRQNLPEHTQGLGSKW 60
Db 1 MWTLKSSILVLLCLTCSYAFMFSSLRQKTSPPQKVPCEHFRIRQNLPEHTQGLGSKW 60

Qy 61 LWLLFAVVVPFVILKCORDSEKKNKVRMAP 88
Db 61 LWLLXVVVPFVILQCRDSEKKNKQSP 88

RESULT 15
AAG00463
ID AAG00463 standard; protein; 101 AA.
XX
AC AAG00463;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 4544.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX
FN EPI033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GSEST ) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
DR N-PSDB; AAC00469.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 13; SEQ ID NO 4544; 71pp + Sequence Listing; English.
XX
CC The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:16 ; Search time 177.706 Seconds
(without alignments)
248.149 Million cell updates/sec

Title: US-10-092-934-4

Perfect score: 573

Sequence: 1 MWTLKSLVLLCLTCSYAF.....APFLLHHIDSISGVSGKRMF 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	573	100.0	106	14	US-10-138-516-3
2	573	100.0	106	14	US-10-146-130-5
3	573	100.0	106	14	US-10-092-934-4
4	573	100.0	106	14	US-10-153-334-4
5	573	100.0	106	14	US-10-198-069-4
6	573	100.0	106	14	US-10-198-070-4
7	573	100.0	106	14	US-10-294-891-3
8	573	100.0	106	17	US-10-920-313-3
9	453	79.1	171	14	US-10-114-153-30
10	430	75.0	171	16	US-10-821-273-70
11	430	75.0	239	9	US-09-808-701A-28

12	430	75.0	239	14	US-10-233-131-28	Sequence 28, Appl
13	430	75.0	239	15	US-10-240-145-80	Sequence 80, Appl
14	430	75.0	239	15	US-10-262-839-54	Sequence 54, Appl
15	430	75.0	239	18	US-10-291-128-80	Sequence 80, Appl
16	358	62.5	156	14	US-10-114-153-36	Sequence 36, Appl
17	358	62.5	156	14	US-10-114-153-40	Sequence 40, Appl
18	358	62.5	156	14	US-10-114-153-42	Sequence 42, Appl
19	354	61.8	156	14	US-10-114-153-38	Sequence 38, Appl
20	339	59.2	156	14	US-10-114-153-44	Sequence 44, Appl
21	252	44.0	47	14	US-10-114-153-32	Sequence 32, Appl
22	233	40.7	47	14	US-10-114-153-34	Sequence 34, Appl
23	92	16.1	15	14	US-10-294-891-26	Sequence 26, Appl
24	92	16.1	15	17	US-10-920-313-26	Sequence 26, Appl
25	87	15.2	15	14	US-10-294-891-25	Sequence 25, Appl
26	87	15.2	15	17	US-10-920-313-25	Sequence 25, Appl
27	83	14.5	16	14	US-10-294-891-29	Sequence 29, Appl
28	83	14.5	16	17	US-10-920-313-29	Sequence 29, Appl
29	80	14.0	15	14	US-10-294-891-27	Sequence 27, Appl
30	80	14.0	15	17	US-10-920-313-27	Sequence 27, Appl
31	80	14.0	545	15	US-10-112-944-480	Sequence 480, App
32	78.5	13.7	111	17	US-10-732-620-51	Sequence 51, Appl
33	78.5	13.7	111	17	US-10-732-620-52	Sequence 52, Appl
34	78	13.6	15	14	US-10-294-891-28	Sequence 28, Appl
35	78	13.6	15	17	US-10-920-313-28	Sequence 28, Appl
36	77	13.4	15	14	US-10-294-891-24	Sequence 24, Appl
37	77	13.4	15	17	US-10-920-313-24	Sequence 24, Appl
38	76	13.3	15	14	US-10-294-891-23	Sequence 23, Appl
39	76	13.3	15	17	US-10-920-313-23	Sequence 23, Appl
40	74.5	13.0	380	15	US-10-094-749-2909	Sequence 2909, Ap
41	74.5	13.0	470	11	US-09-922-181A-7	Sequence 7, Appli
42	74.5	13.0	544	11	US-09-922-181A-3	Sequence 3, Appli
43	74.5	13.0	683	18	US-10-631-467-660	Sequence 660, App
44	73.5	12.8	217	18	US-10-450-763-34428	Sequence 34428, A
45	73.5	12.8	586	18	US-10-450-763-40995	Sequence 40995, A

ALIGNMENTS

RESULT 1
US-10-138-516-3
; Sequence 3, Application US/10138516
; Publication No. US20030003445A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING ANTIBODIES TO
; TITLE OF INVENTION: NEURAL THREAD PROTEINS
; FILE REFERENCE: 59003.000004
; CURRENT APPLICATION NUMBER: US/10/138,516
; CURRENT FILING DATE: 2002-07-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-516-3

Query Match 100.0%; Score 573; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.3e-60;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MWTLKSLVLLCLTCSYAFMFSLSRQKTSPEQKPCGHEFRIRQNLPEHTQGLGSKW	60
Db	1	MWTLKSLVLLCLTCSYAFMFSLSRQKTSPEQKPCGHEFRIRQNLPEHTQGLGSKW	60
Qy	61	LWLLFAVVPFVLKQDSEKNKVRMAPFFLHHIDISISGVSGKRMF	106
Db	61	LWLLFAVVPFVLKQDSEKNKVRMAPFFLHHIDISISGVSGKRMF	106
RESULT 2			
US-10-146-130-5			


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; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-070-4

Query Match      100.0%; Score 573; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.3e-60;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 LWLLFAVVPFVLKQORDSEKNKVRMAPFFLHHHIDISGVSGKRMF 106
Db 61 LWLLFAVVPFVLKQORDSEKNKVRMAPFFLHHHIDISGVSGKRMF 106

RESULT 7
US-10-294-891-3
; Sequence 3, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GENMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-3

Query Match      100.0%; Score 573; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.3e-60;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSBPQGVPCGEHFRIRQNLPEHTQGLGSKW 60
Db 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSBPQGVPCGEHFRIRQNLPEHTQGLGSKW 60

Qy 61 LWLLFAVVPFVLKQORDSEKNKVRMAPFFLHHHIDISGVSGKRMF 106
Db 61 LWLLFAVVPFVLKQORDSEKNKVRMAPFFLHHHIDISGVSGKRMF 106

RESULT 8
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; Sequence 3, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GENMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-3

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Qy 61 LWLLFAVVPFVLKQORDSEKNKVRMAPFFLHHHIDISGVSGKRMF 106
Db 61 LWLLFAVVPFVLKQORDSEKNKVRMAPFFLHHHIDISGVSGKRMF 106

RESULT 9
US-10-114-153-30
; Sequence 30, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennnda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACI
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
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; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 30
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-153-30

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QY 61 LWLLFAVVPFVLKCORDSEKKNKVRMAP 88
DB 61 LWLLFAVVPFVLKCORDSEKKNKVRMAP 88

RESULT 10
US-10-821-273-70
; Sequence 70, Application US/10821273
; Publication No. US20040248256A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steinger II, Robert J.
; APPLICANT: Bowman, Michael R.
; APPLICANT: Diblasio-Smith, Elizabeth
; APPLICANT: Widom, Angela
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000101.
; CURRENT APPLICATION NUMBER: US/10/821,273
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US 09/306,111
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 60/084,564
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: US 60/087,645
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: US 60/093,712
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 60/094,935
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 60/095,880
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/096,068
; PRIOR FILING DATE: 1998-08-11
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 70
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-273-70

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Best Local Similarity 90.9%; Pred. No. 1.2e-42;
Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

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DB 1 MWTLKSSLVLLCLCTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60

QY 61 LWLLFAVVPFVLKCORDSEKKNKVRMAP 88
DB 61 LWLLFAVVPFVLKCORDSEKKNKVRMAP 88

RESULT 11
US-09-808-701A-28
; Sequence 28, Application US/09808701A
; Publication No. US20020146757A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6610536el Nucleic Acids and
; FILE REFERENCE: 790CIP2D
; CURRENT APPLICATION NUMBER: US/09/808,701A
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 28
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-701A-28

Query Match          75.0%; Score 430; DB 9; Length 239;
Best Local Similarity 90.9%; Pred. No. 1.8e-42;
Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MWTLKSSLVLLCLCTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
DB 69 MWTLKSSLVLLCLCTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 128

QY 61 LWLLFAVVPFVLKCORDSEKKNKVRMAP 88
DB 129 LWLLFAVVPFVLKCORDSEKKNKVRMAP 156

RESULT 12
US-10-233-131-28
; Sequence 28, Application US/10233131
; Publication No. US20030096279A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Ren, Felyan
; APPLICANT: Wang, Dunrui
; APPLICANT: Chen, Rui-hong
```

APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030096279A1el Nucleic Acids and
FILE REFERENCE: 790CIP2D DIVA
CURRENT APPLICATION NUMBER: US/10/233,131
CURRENT FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Pt_FL_genes Version 2.0
SEQ ID NO 28
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-10-233-131-28

Query Match 75.0%; Score 430; DB 14; Length 239;
Best Local Similarity 90.9%; Pred. No. 1.8e-42;
Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MWTLKSSIVLLCLTCSYAFMFSSLRKTSPPQGVPCGGEHFRIRQNLPEHTQGLGSKW 60
Db 69 MWTLKSSIVLLCLTCSYAFMFSSLRKTSPPQGVPCGGEHFRIRQNLPEHTQGLGSKW 128

Qy 61 LWLFAVVVPFVILKCORDSEKNKVRMAP 88
Db 129 LWLFAVVVPFVILKCORDSEKNKEQSPP 156

RESULT 13
US-10-240-145-80
Sequence 80, Application US/10240145
Publication No. US20030235883A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
CURRENT APPLICATION NUMBER: US/10/240,145
CURRENT FILING DATE: 2002-09-27
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 172
SOFTWARE: Custom
SEQ ID NO 80
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-10-240-145-80

Query Match 75.0%; Score 430; DB 15; Length 239;
Best Local Similarity 90.9%; Pred. No. 1.8e-42;
Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MWTLKSSIVLLCLTCSYAFMFSSLRKTSPPQGVPCGGEHFRIRQNLPEHTQGLGSKW 60
Db 69 MWTLKSSIVLLCLTCSYAFMFSSLRKTSPPQGVPCGGEHFRIRQNLPEHTQGLGSKW 128

Qy 61 LWLFAVVVPFVILKCORDSEKNKVRMAP 88
Db 129 LWLFAVVVPFVILKCORDSEKNKEQSPP 156

Db 129 LWLFAVVVPFVILKCORDSEKNKEQSPP 156

RESULT 14
US-10-262-839-54
Sequence 54, Application US/10262839
Publication No. US20040038877A1
GENERAL INFORMATION:
APPLICANT: Alsbrook, John.
APPLICANT: Anderson, David W.,
APPLICANT: Boldog, Ferenc,
APPLICANT: Burgess, Catherine,
APPLICANT: Catterton, Elina,
APPLICANT: Edinger, Shlomit,
APPLICANT: Ellerman, Karen,
APPLICANT: Gerlach, Valerie,
APPLICANT: Gorman, Linda,
APPLICANT: Guo, Xiaojia,
APPLICANT: Ji, Weizhen,
APPLICANT: Kekuda, Ramesh,
APPLICANT: Leach, Martin,
APPLICANT: Li, Li,
APPLICANT: Miller, Charles,
APPLICANT: Patturajan, Meera,
APPLICANT: Reiger, Daniel,
APPLICANT: Rothenberg, Mark,
APPLICANT: Shimkets, Richard,
APPLICANT: Smithson, Glennda,
APPLICANT: Spytek, Kimberly,
APPLICANT: Taupier, Raymond, Jr.,
APPLICANT: Vernet, Corine,
APPLICANT: Voss, Edward,
APPLICANT: Zerhusen, Brian,
APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-462A
CURRENT APPLICATION NUMBER: US/10/262,839
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,101
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/371,972
PRIOR FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: 60/327,342
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/328,044
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,849
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/374,738
PRIOR FILING DATE: 2002-04-23
Remaining Prior Application data removed - See File wrapper or PALM.
NUMBER OF SEQ ID NOS: 367
SOFTWARE: Curaseq1ist version 0.1
SEQ ID NO 54
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-839-54

Query Match 75.0%; Score 430; DB 15; Length 239;
Best Local Similarity 90.9%; Pred. No. 1.8e-42;
Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MWTLKSSIVLLCLTCSYAFMFSSLRKTSPPQGVPCGGEHFRIRQNLPEHTQGLGSKW 60
Db 129 LWLFAVVVPFVILKCORDSEKNKEQSPP 156

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Db      69  MWTLKSSVLLCLCTCSYAFMFSSURQKTSPEQGVQVGBHFRIQNLPHTQGLGSKW 128

Qy      61  LMLLFAWPFVILKCQDSEKKNKVMAP 88
         ||||| |||||:|||||:|
Db      129 LMLLFWVPFVILQCDSEKKEQSP 156

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RESULT 15

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US-10-291-128-80
; Sequence 80, Application US/10291128
; Publication No. US2005020422A1
; GENERAL INFORMATION:
; APPLICANT: Nuvelo, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP4
; CURRENT APPLICATION NUMBER: US/10/291.128
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/10484
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/668,680
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/695,618
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 09/728,711
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 09/808,701
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: Custom
; SEQ ID NO 80
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-128-80

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Query Match 75.0%; Score 430; DB 18; Length 239;
Best Local Similarity 90.9%; Pred. No. 1.8e-42;
Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy	1	MWTLKASLVLLCLTCSYAFNPSSLRKTSPOGKVCGBHFRIQNLPHHTQGLGSKW	60
Db	69	MWTLKASLVLLCLTCSYAFNPSSLRKTSPOGKVCGBHFRIQNLPHHTQGLGSKW	128
Qy	61	LWLLFAVVPFVILKCQDSEKNKVRMAP	88
Db	129	LWLLFAVVPFVILQCQDSEKNKQESPP	156

Search completed: October 11, 2005, 07:39:44
Job time : 178.706 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:19 ; Search time 24.2326 Seconds
(without alignments)
326.535 Million cell updates/sec

Title: US-10-092-934-4
Perfect score: 573
Sequence: 1 MWTLKSLVLLCLTCSYAF.....APFLHIDSIGVGKRMF 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	430	75.0	239	4	US-09-808-701A-28
2	423	73.8	101	4	US-09-513-999C-4544
3	422	73.6	138	4	US-09-621-976-3898
4	74.5	13.0	698	4	US-09-949-016-11419
5	69	12.0	248	4	US-09-270-767-44243
6	68	11.9	1125	4	US-09-949-016-10194
7	67	11.7	508	4	US-09-328-352-6467
8	66.5	11.6	1021	4	US-09-252-991A-19205
9	66	11.5	733	4	US-09-949-016-7651
10	65.5	11.4	270	4	US-09-107-532A-5444
11	65.5	11.4	364	4	US-09-270-767-42122
12	65	11.3	625	4	US-09-949-016-9694
13	64	11.2	421	4	US-09-252-991A-17417
14	64	11.2	810	4	US-09-538-092-1275
15	63.5	11.1	639	4	US-09-949-016-9434
16	63.5	11.1	685	4	US-09-538-092-956
17	63.5	11.1	1290	4	US-09-949-016-8627
18	63.5	11.1	1312	4	US-09-949-016-10141
19	62.5	10.9	403	4	US-10-017-372E-21
20	62.5	10.9	407	4	US-10-017-372E-21
21	62	10.8	542	4	US-09-389-956-78
22	62	10.8	714	4	US-09-492-709A-253
23	62	10.8	733	4	US-09-489-039A-12568
24	61	10.6	285	1	US-08-292-045-5
25	61	10.6	543	4	US-09-362-123A-4
26	60.5	10.6	173	1	US-08-157-005-8
27	60.5	10.6	173	2	US-08-799-464A-24

28	60.5	10.6	173	3	US-08-747-863-8	Sequence 8, Appli
29	60.5	10.6	173	4	US-09-565-864-8	Sequence 8, Appli
30	60.5	10.6	173	4	US-08-301-435-24	Sequence 24, Appli
31	60.5	10.6	173	4	US-10-226-065-8	Sequence 8, Appli
32	60.5	10.6	173	5	PCT-US95-09927-24	Sequence 24, Appli
33	60.5	10.6	173	5	PCT-US95-10904-24	Sequence 24, Appli
34	60.5	10.6	295	2	US-08-481-956A-9	Sequence 9, Appli
35	60.5	10.6	295	2	US-08-629-291A-9	Sequence 9, Appli
36	60.5	10.6	295	2	US-08-658-335B-9	Sequence 9, Appli
37	60.5	10.6	295	4	US-09-406-640-9	Sequence 9, Appli
38	60.5	10.6	642	4	US-09-949-016-6986	Sequence 6986, Ap
39	60.5	10.6	648	4	US-09-949-016-10374	Sequence 10374, A
40	60.5	10.6	1214	4	US-09-949-016-6885	Sequence 6885, Ap
41	60.5	10.6	1318	4	US-09-949-016-7130	Sequence 7130, Ap
42	60.5	10.6	1464	1	US-08-026-138E-1	Sequence 1, Appli
43	60.5	10.6	1464	3	US-08-436-332B-10	Sequence 10, Appli
44	60.5	10.6	1464	4	US-08-217-704C-2	Sequence 2, Appli
45	60.5	10.6	1464	4	US-09-949-016-8311	Sequence 8311, Ap

ALIGNMENTS

RESULT 1

US-09-808-701A-28
; Sequence 28, Application US/09808701A
; Patent No. 6610536
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6610536el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 790CIP2D
; CURRENT APPLICATION NUMBER: US/09/808,701A
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 28
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-701A-28

Query Match 75.0%; Score 430; DB 4; Length 239;
Best Local Similarity 90.9%; Pred. No. 1.7e-46;
Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy	1	MWTLKSLVLLCLTCSYAFMFSSLRKTSPOQKQVGEHFRIRQNLPEHTQGLGSKW	60
Db	69	MWTLKSLVLLCLTCSYAFMFSSLRKTSPOQKQVGEHFRIRQNLPEHTQGLGSKW	128
Qy	61	LWLLFAVVPFVILKCRDSEKNKVRMAP	88
Db	129	LWLLFAVVPFVILKCRDSEKNKQSP	156

RESULT 2

US-09-513-999C-4544
; Sequence 4544, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG

Query Match	11.7%	Score 67;	DB 4;	Length 508;	
Best Local Similarity	24.4%;	Pred. No. 6.5;			
Matches	19;	Conservative 15;	Mismatches 34;	Indels 10;	Gaps 2;
Qy	2	WTKSSVLLLCGLCSVAFMFSSLRQKTSBPQGVKPCGEHFRIRONLPEHTQGWLGSKWL	61		
		: : : : : : : : : : : : : : : : : :			
Db	402	FTIISALTSILCITFMVLVLSYIYRKKSP-----LHQSKYKMP-----GGFLFMAWM	451		
Qy	62	WLLFAVVPFVILKCQDS	79		
		: : : : : : : : : : : : : : : : : :			
Db	452	TMLFLVFTIVIALDHDHT	459		

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Query Match      11.5%; Score 66; DB 4; Length 733;  
Best Local Similarity 27.2%; Pred. No. 14;  
Matches 25; Conservative 14; Mismatches 31; Indels 22; Gaps 5  
  
Qy .. 12 LCLTCSYAF-WFSSLRKQTSPQKV-----CGEHFRIRQLPHTQNLGSKMLWLLF 65  
       :|||::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db    511 VCFCSHAFTQANLNMHLRTHTEKPKQCHLGKTFRTQASLDKHNRHHTGTGER----- 564  
  
Qy   66 AVPFVILKC--QRDSEKNKVRMAFFFLHHIDS 96  
  
Db   565 ---PFSCEFCFORFTEKGPL-----LRHVAS 587
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; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17417
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17417

Query Match      11.2%; Score 64; DB 4; Length 421;
Best Local Similarity 44.7%; Pred. No. 12;
Matches 17; Conservative 5; Mismatches 12; Indels 4; Gaps 1;

Qy 31 EPQGVKPCGHEFRIRQNLPEHTQGLGSKWLWLLFAVV 68
Db 2 EPPEGSGPHWRVRGLP---CRPGVEALFQLFAVV 35

RESULT 14
US-09-538-092-1275
; Sequence 1275, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratPatSeqformatter Version 0.9
; SEQ ID NO 1275
; LENGTH: 810
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q06730
US-09-538-092-1275

Query Match      11.2%; Score 64; DB 4; Length 810;
Best Local Similarity 27.8%; Pred. No. 28;
Matches 22; Conservative 10; Mismatches 31; Indels 16; Gaps 4;

Qy 13 CLTCSYAFMFSS---LRQKTS---EPQGVKPCGHEFRIRQNLPEHTQGLGSKWLWLLFA 66
Db 414 CNACGKTFQCKSDLTGKQRTHTGLKPYECYCGSKSFRVTSHLKVHQRTHGTGEK----- 466

Qy 67 VVPFVILKCORD-SEKNKV 84
Db 467 --PFECLCGKSFSEKSNL 483

RESULT 15
US-09-949-016-9434
; Sequence 9434, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9434
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9434

Query Match      11.1%; Score 63.5; DB 4; Length 639;
Best Local Similarity 25.3%; Pred. No. 24;
Matches 19; Conservative 12; Mismatches 29; Indels 15; Gaps 3;

Qy 13 CLTCSYAFMF-SSLRQKTSBPQGVKVP-----CGEHFRIRQNLPEHTQGLGSKWLWLLFA 66
Db 416 CKECGKSFYNSLSLTHEVRTHTEIPEYECNECGKAFKYSSSLTYCHMIHTGEK----- 468

Qy 67 VVPFVILKCORDSEK 81
Db 469 --PPECNECGKAFSK 481

Search completed: October 11, 2005, 07:42:49
Job time : 26.2326 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 16.4385 Seconds
(without alignments)
620.432 Million cell updates/sec

Title: US-10-092-934-5
Perfect score: 582
Sequence: 1 MFFVLRFRCFFETESHSL.....VQGGKQKLYISADLVHLIA 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: PIR1.*
- 2: PIR2.*
- 3: PIR3.*
- 4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	183.5	31.5	613	4 C40201	artifact-warning s
2	161.5	27.7	673	4 F40201	artifact-warning s
3	158	27.1	627	4 A40201	artifact-warning s
4	145	24.9	46	2 I54375	gene NF2 protein -
5	135	23.2	39	2 I54374	gene NF2 protein -
6	132	22.7	53	2 A42442	integrin beta-1 ch
7	108	18.6	597	4 E40201	artifact-warning s
8	104	17.9	100	2 A46010	X-linked retinopat
9	92	15.8	522	2 T08711	gamma-adaptin homo
10	90	15.5	440	2 A26359	decay-accelerating
11	86	14.8	773	2 T00502	probable receptor-
12	73.5	12.6	588	2 E96633	probable Serine/Th
13	72.5	12.5	447	2 A96639	protein t1f9.18 [i
14	71	12.2	652	2 T10576	hypothetical prote
15	71	12.2	766	2 B85440	receptor kinase-li
16	71	12.2	2302	2 T14328	protein-tyrosine-p
17	70	12.0	668	2 T26724	hypothetical prote
18	70	12.0	907	2 T04820	aconitate hydratase
19	68.5	11.8	2183	2 T42764	coagulation factor
20	68	11.7	4302	2 A38971	polycystic kidney
21	67.5	11.6	130	2 B72702	hypothetical prote
22	67.5	11.6	854	1 QRHYLD	LDL receptor precu
23	67.5	11.6	879	1 QRTTLD	LDL receptor precu
24	66.5	11.4	556	2 T24690	hypothetical prote
25	65.5	11.3	1192	2 T48499	receptor-like prot
26	65	11.2	424	2 JC5921	non-selective cati
27	65	11.2	898	2 T10101	aconitate hydratase
28	64.5	11.1	321	2 I61749	pheromone receptor
29	64.5	11.1	356	2 A11954	hypothetical prote

30	64.5	11.1	520	2 S14600	E2 glycoprotein pr
31	64.5	11.1	593	1 GYHU	granulin precursor
32	64.5	11.1	980	2 T05414	protein kinase hom
33	64	11.0	507	2 H82378	probable long-chai
34	63.5	10.9	427	2 A71612	translation releas
35	63.5	10.9	454	2 T42680	hypothetical prote
36	63.5	10.9	2529	2 A56923	transcription fact
37	63.5	10.9	2578	2 A56922	transcription fact
38	63	10.8	331	2 T31998	hypothetical prote
39	63	10.8	386	2 AG0081	conserved hypothet
40	63	10.8	837	1 A29512	LDL receptor precu
41	62.5	10.7	236	2 S31058	hypothetical prote
42	62.5	10.7	329	1 A48754	B7-2 antigen - hum
43	62.5	10.7	606	2 S35427	env polypeptid -
44	62.5	10.7	640	2 F75553	hypothetical prote
45	62.5	10.7	647	2 T35931	probable gamma-glu

ALIGNMENTS

RESULT 1

C40201
artifact-warning sequence (translated ALU class C) - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C:Accession: C40201
R:Claverie, J.M.
personal communication, 1992
A:Reference number: A40201
A:Accession: C40201
A:Molecule type: DNA
A:Residues: 1-613 <CLA>
R:Claverie, J.M.
Genomics 12, 838-841, 1992
A:Title: Identifying coding exons by similarity search: Alu-derived and other potential
A:Reference number: A40200; MUID:92241891; PMID:1572661
A:Contents: annotation
C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames of o
in-frame stop codons are shown as 'X'.
C:Comment: Any significant similarity of a predicted protein sequence to a portion of th

Query Match	31.5%	Score 183.5;	DB 4;	Length 613;
Best Local Similarity	62.3%;	Pred. No. 3.2e-12;		
Matches	38;	Conservative	4;	Mismatches 16;
				Indels 3;
				Gaps 2;
Qy	8	FCFCFFETESHSLTQAGVQWCELGSPOLPSGFKRFSCLSLSSWDSHEPHP--VICS	65	
Db	310	FFFFFETESHVTOAGVQWRDLGSLQAPPPGPFSCLSLRTWDY-RRPHHAQLIFCI	368	
Qy	66	F 66		
Db	369	F 369		

RESULT 2

F40201
artifact-warning sequence (translated ALU class F) - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C:Accession: F40201
R:Claverie, J.M.
personal communication, 1992
A:Reference number: A40201
A:Accession: F40201
A:Molecule type: DNA
A:Residues: 1-673 <CLA>
R:Claverie, J.M.
Genomics 12, 838-841, 1992
A:Title: Identifying coding exons by similarity search: Alu-derived and other potential
A:Reference number: A40200; MUID:92241891; PMID:1572661
A:Contents: annotation

R; Theologians, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huizar, L.; Nature 408, 816-820, 2000

C.A.; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

T10576
hypothetical protein F25P4.180 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse ear cross)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #T10576
C:Accession: T10576
R:Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Raju,
submitted to the Protein Sequence Database, June 1999
A:Reference number: T10576

R; Theologians, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huizar, L.; Nature 408, 816-820, 2000

C.A.; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

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Result No.	Score	Query *		DB	ID	Description
		Match	Length			
1	234.5	40.3	375	2	O60448	homo sapien
2	220.5	37.9	124	2	O6ZVF6	homo sapien
3	211	36.3	132	2	O6ZNU7	homo sapien
4	207	35.6	131	2	O6ZTD3	homo sapien
5	203	34.9	135	2	O6ZFK1	macaca fasc
6	203	34.9	151	2	O9HA67	homo sapien
7	203	34.9	165	2	O6ZS53	homo sapien
8	203	34.9	165	2	O6ZT71	homo sapien
9	203	34.9	195	2	O6ZUW2	homo sapien
10	201	34.5	124	2	O6ZSG7	homo sapien
11	201	34.5	158	2	O8NAL9	homo sapien
12	201	34.5	176	2	O6ZTU6	homo sapien
13	200	34.4	165	2	O6ZS21	homo sapien
14	199.5	34.3	591	1	ALU6 HUMAN	homo sapien
15	199	34.2	122	2	O6ZVH4	homo sapien
16	198	34.0	299	2	O6ZRN6	homo sapien
17	196.5	33.8	170	2	O6ZV14	homo sapien
18	196	33.7	129	2	O6ZS06	homo sapien
19	194.5	33.4	152	2	O9NX85	homo sapien
20	192.5	33.1	117	2	O8U002	homo sapien
21	192	33.0	61	2	O9U148	homo sapien
22	192	33.0	151	2	O8N287	homo sapien
23	191.5	32.9	137	2	O6ZS97	homo sapien
24	191	32.8	132	2	O6ZS28	homo sapien
25	190.5	32.7	129	2	O6ZW43	homo sapien
26	189	32.5	163	2	O96MM0	homo sapien
27	188	32.3	123	2	O6ZMQ3	homo sapien
28	187	32.1	102	2	O9P147	homo sapien
29	187	32.1	593	1	ALU6 HUMAN	homo sapien
30	186	32.0	83	2	O961D7	homo sapien
31	186	32.0	120	2	O6ZSU7	homo sapien


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Q9HA67
ID Q9HA67 PRELIMINARY; PRT; 151 AA.
AC Q9HA67;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ12155.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN MIM:606400
PP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe K., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugeno J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs";
RL Natl. Genet. 36:40-45(2004).
DR EMBL; AK022217; BAB13989.1; --
SQ SEQUENCE 151 AA; 16972 MW; ECE65BBD50DF2811 CRC64;

Query Match 34.9%; Score 203; DB 2; Length 151;
Best Local Similarity 54.5%; Pred. No. 2.3e-14;
Matches 42; Conservative 5; Mismatches 10; Indels 20; Gaps 3;

Qy 9 CFC-----FFETESHSLTQAGVQWCELGSPQPLPSGFKRFSCLSLSSWDYSHE 57
Db 12 CICKHYAPPTAPHLPPFETESHVSHTQAGVQWCDLGLSLQSPGPKQFSCLSLSRSWDYRV 71

Qy 58 PPHPVIC-----SFLME 69
Db 72 P-----LCLANFIVFLVE 84

RESULT 7
ID Q6ZS53 PRELIMINARY; PRT; 165 AA.
AC Q6ZS53;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ45823.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
RN MIM:606400
PP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe K., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugeno J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs";
RL Natl. Genet. 36:40-45(2004).
DR EMBL; AK022217; BAB13989.1; --
SQ SEQUENCE 151 AA; 16972 MW; ECE65BBD50DF2811 CRC64;

Query Match 34.9%; Score 203; DB 2; Length 165;
Best Local Similarity 56.8%; Pred. No. 2.5e-14;
Matches 42; Conservative 7; Mismatches 23; Indels 2; Gaps 2;

Qy 1 MPFVLYRFCFC-PPETESHSLTQAGVQWCELGSPQPLPSGFKRFSCLSLSSWDYSHEPP 59
Db 59 VFFPFFYLFSPFPETESLSVAQAGVQWHDGLSLQPRPPGPKQFSCLSLSPSSWDYGHPTPQ 118

Qy 60 HPV-ICSFLEMEKCL 72
Db 119 RSANFCIFRKDRVL 132

RESULT 8
ID Q6ZT71 PRELIMINARY; PRT; 165 AA.
AC Q6ZT71;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ44907.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN MIM:606400
PP SEQUENCE FROM N.A.
RC TISSUE=Amnion;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
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RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
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RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
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RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe K., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugeno J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs";
RL Natl. Genet. 36:40-45(2004).
DR EMBL; AK126855; BAC86723.1; --
SQ SEQUENCE 165 AA; 19309 MW; 2BBEB4386467B575 CRC64;

Query Match 34.9%; Score 203; DB 2; Length 165;
Best Local Similarity 56.8%; Pred. No. 2.5e-14;
Matches 42; Conservative 7; Mismatches 23; Indels 2; Gaps 2;

Qy 1 MPFVLYRFCFC-PPETESHSLTQAGVQWCELGSPQPLPSGFKRFSCLSLSSWDYSHEPP 59
Db 59 VFFPFFYLFSPFPETESLSVAQAGVQWHDGLSLQPRPPGPKQFSCLSLSPSSWDYGHPTPQ 118

Qy 60 HPV-ICSFLEMEKCL 72
Db 119 RSANFCIFRKDRVL 132

RESULT 9
ID Q6ZUW2 PRELIMINARY; PRT; 195 AA.
AC Q6ZUW2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ43278.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagaatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.,
RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK125268; BAC86106.1; -.
DR EMBL; AK125268; BAC86106.1; -.
SQ SEQUENCE 195 AA; 21399 MW; 6C422556FE990B1 CRC64;

Query Match      34.9%; Score 203; DB 2; Length 195;
Best Local Similarity 51.1%; Pred. No. 3e-14;
Matches 47; Conservative 7; Mismatches 26; Indels 12; Gaps 3;

QY 4 VLYRFCFFETESHLSLTQAGVQVCELGSPQPLSPGKFRFSCLSLSSWDYSHEPPHPV- 62
DB 77 ILGLFVILFFETESHVTSQAGVQVCELGSLQPLPPGKFRFSCLSLSSWDYRRVPPHPAS 136
QY 63 ICSPFLMEK-----CLILKPNQDITGPI 85
DB 137 LPFLMPKRYYYIYLFCTLL--PVLDLSGTI 166

RESULT 10
ID Q6ZSG7 PRELIMINARY; PRT; 124 AA.
AC Q6ZSG7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ45543.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thalamus;
RA Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagaatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahara K.,
RA Masuho Y., Nagai K., Isogai T.;
RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK127451; BAC86986.1; -.
DR EMBL; AK127451; BAC86986.1; -.
SQ SEQUENCE 124 AA; 14502 MW; 07D5313B6E1DE897 CRC64;

Query Match      34.58%; Score 201; DB 2; Length 124;
Best Local Similarity 63.2%; Pred. No. 3.1e-14;
Matches 36; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 5 LYRFCFFETESHLSLTQAGVQVCELGSPQPLSPGKFRFSCLSLSSWDYSHEPPHP 61
DB 1 MWFFVILFETESHVTSQAGVQVCELGSLQPLPPGKFRFSCLSLSSWDYRRVPPHP 57

RESULT 11
Q8NAL9 PRELIMINARY; PRT; 158 AA.
AC Q8NAL9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

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DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ35131.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Oabayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK092450; BAC03893.1; -.
SQ SEQUENCE 158 AA; 17414 MW; E151503015F2FE34 CRC64;

Query Match      34.5%; Score 201; DB 2; Length 158;
Best Local Similarity 67.8%; Pred. No. 4e-14;
Matches 40; Conservative 2; Mismatches 13; Indels 4; Gaps 1;

QY 16 ESHSLTQAGVQVCELGSPQPLSPGKFRFSCLSLSSWDYSHEPPP-----HPVICSPFLMEK 70
DB 2 ESHSVTQAGVQVCELGSLQPLPPGKFRFSCLSLSSWDYRRVPPPLANFCIFPSFFFEK 60

RESULT 12
Q6ZTU6 PRELIMINARY; PRT; 176 AA.
ID Q6ZTU6;
AC Q6ZTU6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ44211.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
RA Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,
RA Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,

```


Db 496 FFETESRVAQAQGVQWRDLGSLQPPPGFKRFSCLSLPSSWDYRRAPPPRPNFCIF 551

RESULT 15

Q6ZVH4

ID Q6ZVH4 PRELIMINARY; PRT; 122 AA.

AC Q6ZVH4;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein FLJ42572.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Cerebellum;

RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,

RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,

RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,

RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,

RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,

RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,

RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,

RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,

RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL: AK124563; BAC85887.1; -

SQ SEQUENCE 122 AA; 13547 MW; 39472EF24DED96D3 CRC64;

Query Match

Best Local Similarity 34.2%; Score 199; DB 2; Length 122;

Matches 48; Conservative 47.1%; Pred. No. 5e-14;

Matches 48; Conservative 7; Mismatches 27; Indels 20; Gaps 4;

Qy 1 MFFVLVRFCTCFPETHSHLTQAGVQWCELGSPQLPSGPKRFSCLSLSSWDYSHEPPH 60

Db 21 IFFFLF-----FIETESRVAQAQGVQWCDLSLSLQPPPGFKRFSCLSLPSSWDYRCPPPR 75

Qy 61 PV-ICSFLEKCLILYKPNGDTIGPILVQQGKQKLYISADL 101

Db 76 LVTFCIFSRDRVSSCW-PGG-----LKLITSGDL 103

Search completed: October 11, 2005, 07:18:46

Job time : 64.6283 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 78.508 Seconds
(without alignments)
522.196 Million cell updates/sec

Title: US-10-092-934-5
Perfect score: 582
Sequence: 1 MFVLYRFCFFETESHSL.....VQQKQKLYISADLVHLIA 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_l6Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	582	100.0	106	Aae29146	Neural th
2	582	100.0	106	ABr63244	106 amino
3	582	100.0	106	ABU02976	Human neu
4	582	100.0	106	Aae33193	Neural th
5	582	100.0	106	ABj19449	106-mer n
6	582	100.0	106	ABj19449	AD7C-neur
7	237.5	40.8	119	Aao06149	Human pol
8	234.5	40.3	85	ABb28760	Peptide #
9	234.5	40.3	375	ABb01399	Neuron-as
10	234.5	40.3	375	ABb81538	Neural th
11	234.5	40.3	375	Aae29142	AD7C-NTP
12	234.5	40.3	375	ABr63268	AD7C-neur
13	234.5	40.3	375	ADA84017	Human POM
14	234.5	40.3	375	ABU03024	Human neu
15	234.5	40.3	375	ABb99774	Amino aci
16	234.5	40.3	375	ABj19445	AD7C-neur
17	234.5	40.3	375	ADB37642	Human neu
18	234.5	40.3	375	ADR14409	Human NP-
19	231.5	39.8	76	ABb75336	Gene 47 h
20	230.5	39.6	89	ABG09800	Novel hum
21	230.5	39.6	123	ABb63958	Human pro
22	226	38.8	97	ABb11638	Human sec
23	223.5	38.4	100	ADA55476	Human pro
24	223.5	38.4	396	AAU30455	Novel hum
25	223	38.3	133	ABb97994	Human cyc

26	221	38.0	168	5	ADK34256	Novel hum
27	221	38.0	1026	6	ABU12314	Human PAT
28	220.5	37.9	124	8	ADQ65229	Novel hum
29	219	37.6	131	4	AAU32027	Novel hum
30	218.5	37.5	101	6	ADA54613	Human pro
31	218	37.5	861	6	ABU12316	Human PAT
32	218	37.5	895	6	ABU12304	Human PAT
33	218	37.5	933	6	ABU12307	Human PAT
34	218	37.5	993	6	ABU12300	Human PAT
35	218	37.5	1044	6	ABU12310	Human PAT
36	217.5	37.4	92	5	ADK34934	Novel hum
37	215.5	37.0	146	4	ABG08195	Novel hum
38	215.5	37.0	219	4	AAG66500	Human neu
39	215.5	37.0	433	7	ADC87285	Human GPC
40	214.5	36.9	114	7	ADB64269	Human pro
41	214	36.8	397	2	AAR95913	Neural th
42	213.5	36.7	129	4	AAO08006	Human pol
43	213	36.6	132	4	ABG08282	Novel hum
44	212.5	36.5	92	5	ABb99219	Human try
45	212.5	36.5	93	4	AAM96679	Human rep

ALIGNMENTS

RESULT 1

AAE29146
ID AAE29146 standard; protein; 106 AA.

XX	AAE29146;				
AC					
XX					
DT	27-JAN-2003	(first entry)			
XX					
DE	Neural thread protein (NTP) #4.				
XX					
KW	Neural thread protein; NTP; hyperplasia; hypertrophy; arteriosclerosis;				
KW	haemorrhoid; gene therapy; tumour; vascular disease; atherosclerosis;				
KW	inflammatory disease; nutritional deficiency disease; genetic disease;				
KW	autoimmune disease; metabolic disease; traumatic disease; intoxication;				
KW	infectious disease; congenital malformation; enzyme deficiency disease;				
KW	amyloid disease; fibrosis disease; storage disease; radiation disease;				
KW	poisoning; environmental disease; endocrine disease; protein therapy;				
KW	degenerative disease; mechanical disease.				
XX	Unidentified.				
OS					
XX					
PN	WO200274323-A2.				
XX					
PD	26-SEP-2002.				
XX					
PF	08-MAR-2002; 2002WO-IB001959.				
XX					
PR	08-MAR-2001; 2001US-0273957P.				
XX					
PA	(AVER/) AVERBACK P.				
XX					
PI	Averback P;				
XX					
DR	WPI; 2002-759864/82.				
XX					
PT	Treating a condition in a patient requiring removal or destruction of				
PT	cells, such as a benign or malignant tumor of a tissue or an inflammatory				
PT	disease, comprises administering a neural thread protein (NTP) or a NTP				
PT	gene to a mammal.				
XX					
PS	Claim 23; Fig 5; 70pp; English.				
XX					
CC	The invention relates to a method for treating a condition in a patient				
CC	requiring removal or destruction of cells. The method involves				
CC	administering to a mammal a neural thread protein (NTP), or administering				
CC	to a tumour or other target cell a NTP gene, where the expression of the				
CC	NTP gene is induced resulting in expression of the NTP protein. The				
CC	method and NTP are useful for treating a condition in a patient requiring				

CC removal or destruction of cells, such as a benign or malignant tumour of
CC a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue,
CC preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,
CC bacterially, or parasitically altered tissue, or a malformation of a
CC tissue. Other conditions include a cosmetic modification to a tissue,
CC such as removal of unwanted facial hair, warts or unwanted fatty tissue,
CC a vascular disease, particularly atherosclerosis or arteriosclerosis,
CC haemorrhoids, or varicose veins, an inflammatory disease, autoimmune
CC disease, metabolic disease, hereditary/genetic disease, traumatic disease
CC or physical injury, nutritional deficiency disease, infectious disease,
CC congenital malformation, amyloid disease, fibrosis disease, storage
CC disease, enzyme deficiency disease, poisoning, intoxication, degenerative
CC disease, radiation disease, environmental disease, endocrine disease or
CC mechanical disease. The invention is useful in protein therapy and gene
CC therapy. The present sequence is NTP protein
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 582; DB 5; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.1e-63;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFFVLYRFCFCFFETESHSLTQAGVQWVCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60
DB 1 MFFVLYRFCFCFFETESHSLTQAGVQWVCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60
QY 61 PVICSFMEKCLILYKPNGDTIGPILVQOGKROKLYISADLVHLIA 106
DB 61 PVICSFMEKCLILYKPNGDTIGPILVQOGKROKLYISADLVHLIA 106

RESULT 2

ABR63244
ID ABR63244 standard; protein; 106 AA.

XX ABR63244;

XX 28-AUG-2003 (first entry)

DE 106 amino acid neural thread protein.

XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;

KW neural thread protein; NTP; tumour.

XX Unidentified.

XX WO2003008443-A2.

PN 30-JAN-2003.

XX 19-JUL-2002; 2002WO-CA001105.

PR 19-JUL-2001; 2001US-0306150P.

PR 19-JUL-2001; 2001US-0306161P.

PR 16-NOV-2001; 2001US-0331477P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

PI WPI; 2003-247999/24.

XX Novel neural thread protein peptide, referred as cell death peptide,
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.

XX Disclosure; Fig 5; 77pp; English.

XX The present invention relates to a neural thread protein (NTP) peptide
CC referred to as cell death peptide. Thought to be cytostatic,
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC treating a condition in a patient requiring removal or destruction of
CC cells, for treating a condition such as benign or malignant tumor,

CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for
CC a pancreatic thread protein. The peptide is conjugated, linked or bound
CC to a molecule chosen from antibody or its fragment, antibody-like binding
CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side
CC effects of surgery. The present sequence is an NTP amino acid sequence
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 582; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.1e-63;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFFVLYRFCFCFFETESHSLTQAGVQWVCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60
DB 1 MFFVLYRFCFCFFETESHSLTQAGVQWVCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60
QY 61 PVICSFMEKCLILYKPNGDTIGPILVQOGKROKLYISADLVHLIA 106
DB 61 PVICSFMEKCLILYKPNGDTIGPILVQOGKROKLYISADLVHLIA 106

RESULT 3

ABU02976

ID ABU02976 standard; protein; 106 AA.

XX ABU02976;

XX 20-JAN-2003 (first entry)

XX Human neural thread protein AD7C-NTP, protein fragment #4.

XX Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;
KW transplantation; grafting; chemotherapy; immunotherapy; vaccination;
KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;
KW radiation; tumour; hyperplasia; hypertrophy; overgrowth of tissue;
KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;
KW cosmetic modification; vascular disease; atherosclerosis;
KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;
KW autoimmune disease; metabolic disease; traumatic disease;
KW physical injury; nutritional deficiency disease; infectious disease;
KW amyloid disease; fibrosis disease; storage disease;
KW congenital malformation; enzyme deficiency disease; poisoning;
KW intoxication; environmental disease; radiation disease;
KW endocrine disease; degenerative disease; mechanical disease.

XX Homo sapiens.

XX WO200297030-A2.

XX 05-DEC-2002.

XX 24-MAY-2002; 2002WO-CA000759.

XX 25-MAY-2001; 2001US-0293156P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-041406/03.

XX Novel peptides similar in amino acid sequence to neural thread proteins
PT (NTP), useful for treating unwanted cellular proliferations such as
PT malignant tumors and prostatic hyperplasia.

XX Disclosure; Fig 5; 78pp; English.

XX The invention describes an NTP-peptide (I) comprising at least one amino
CC acid sequence corresponding to part of the amino acid sequence of a
CC neural thread protein, AD7C-NTP. The invention provides a method of

CC treating a condition requiring removal or destruction of cells of a
 CC mammal comprising administering to a mammal, a therapeutic amount of (I).
 CC The treatment is administered to the mammal before, during or after
 CC surgical excision, transplantation, grafting, chemotherapy,
 CC immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,
 CC laser therapy, phototherapy, gene therapy and/or radiation. The method is
 CC useful for treatment of benign or malignant tumour; hyperplasia,
 CC hypertrophy or overgrowth of tissue; virally, bacterially or
 CC parasitically altered tissue; malformation of tissue selected from lung,
 CC breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,
 CC sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary
 CC gland, blood, brain and its coverings, spinal cord, muscle, connective
 CC tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary,
 CC reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,
 CC tonsils, mouth and lymph nodes and lymphoid system; consiliary
 CC hypertrophy; prostatic hyperplasia; cosmetic modification to a tissue;
 CC vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;
 CC varicose veins; inflammatory disease; autoimmune disease; metabolic
 CC disease; hereditary/genetic disease; traumatic disease; physical injury;
 CC nutritional deficiency disease; infectious disease; amyloid disease;
 CC fibrosis disease; storage disease; congenital malformation; enzyme
 CC deficiency disease; poisoning; intoxication; environmental disease;
 CC radiation disease; endocrine disease; degenerative disease and mechanical
 CC disease. This is the amino acid sequence of a human neural thread protein
 CC AD7C-NTP protein fragment
 CC
 CC Sequence 106 AA;

Query Match 100.0%; Score 582; DB 6; Length 106;
 Best Local Similarity 100.0%; Pred. No. 2.1e-63;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MFFVLYRFCFFETESHSLTQAGVQWCELGSPPLPSGFKRFSCLSLSSWDYSHBPPH 60
 Db 1 MFFVLYRFCFFETESHSLTQAGVQWCELGSPPLPSGFKRFSCLSLSSWDYSHBPPH 60
 Qy 61 PVICSFLMEKCLILYKPGNDTIGPILVQOGKQKLYISADLVHLIA 106
 Db 61 PVICSFLMEKCLILYKPGNDTIGPILVQOGKQKLYISADLVHLIA 106

RESULT 4
 AA333193
 ID AA333193 standard; protein; 106 AA.
 AC AA333193;
 XX
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Neural thread protein (NTP) #4.
 XX
 XX Cell death; tissue necrosis; neural thread protein; NTP; amyloidosis;
 KW stroke; brain tumour; Pick's disease; Parkinson's disease; glaucoma;
 KW Alzheimer's disease; gene therapy.
 XX
 OS Unidentified.
 XX
 XX WO200289841-A2.
 XX
 XX 14-NOV-2002.
 XX
 XX 06-MAY-2002; 2002WO-CA000681.
 PF
 XX
 XX 04-MAY-2001; 2001US-0288463P.
 XX
 XX (NYMO-) NYMOX CORP.
 XX
 XX Averbach PA;
 PI
 XX WPI; 2003-120506/11.
 DR
 XX
 XX Preventing, controlling, modulating, ameliorating and/or treating cell
 PT death or tissue necrosis using antibodies to neural thread proteins,

PT useful in disorders such as stroke, brain tumor, glaucoma and Alzheimer's
 PT disease.
 XX
 PS Disclosure; Fig 8; 60pp; English.
 XX
 CC The invention relates to a method of preventing, and/or inhibiting cell
 CC death and/or tissue necrosis in live tissue containing neural thread
 CC proteins (NTP). The method involves contacting the live tissue with at
 CC least one antibody, fragment or derivative that recognises NTP, where the
 CC antibody, fragment or derivative is present to prevent, control,
 CC ameliorate and/or inhibit cell death and/or tissue necrosis caused by the
 CC presence of NTP. Methods and compositions of the invention are useful for
 CC preventing, modulating, controlling and/or treating disorders associated
 CC with cell death and/or tissue necrosis such as stroke, brain tumour,
 CC Pick's disease, Parkinson's disease, amyloidosis, glaucoma and
 CC Alzheimer's disease. The invention is useful in gene therapy. The present
 CC sequence is NTP protein

SQ Sequence 106 AA;

Query Match 100.0%; Score 582; DB 6; Length 106;
 Best Local Similarity 100.0%; Pred. No. 2.1e-63;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFFVLYRFCFFETESHSLTQAGVQWCELGSPPLPSGFKRFSCLSLSSWDYSHBPPH 60
 Db 1 MFFVLYRFCFFETESHSLTQAGVQWCELGSPPLPSGFKRFSCLSLSSWDYSHBPPH 60
 Qy 61 PVICSFLMEKCLILYKPGNDTIGPILVQOGKQKLYISADLVHLIA 106
 Db 61 PVICSFLMEKCLILYKPGNDTIGPILVQOGKQKLYISADLVHLIA 106

RESULT 5
 ABJ19449
 ID ABJ19449 standard; protein; 106 AA.
 XX
 AC ABJ19449;
 XX
 XX 27-MAR-2003 (first entry)
 DT
 XX
 DE 106-mer neural thread protein #2.
 XX
 KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
 KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.
 XX
 OS Unidentified.
 XX
 XX WO200292115-A2.
 XX
 XX 21-NOV-2002.
 PD
 XX
 XX 16-MAY-2002; 2002WO-CA000712.
 PF
 XX
 XX 16-MAY-2001; 2001US-0290971P.
 PR
 XX (NYMO-) NYMOX CORP.
 PA
 XX Averbach PA;
 PI
 XX WPI; 2003-129234/12.
 DR

Preventing and/or inhibiting cell death and/or tissue necrosis in a
 tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
 PT disease, by contacting the live tissue with at least one segment of
 PT neural thread proteins (NTP).
 PT
 XX Disclosure; Fig 5; 60pp; English.
 PS
 XX The invention relates to a novel method for preventing and/or inhibiting
 CC cell death and/or tissue necrosis in a tissue comprising contacting the
 CC live tissue with at least one segment of neural thread proteins (NTP).
 CC The methods are composition are useful for treating a neurodegenerative

CC disorder, such as Alzheimer's disease. This sequence represents an NTP
CC protein of the invention
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 582; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.1e-63;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60
Db 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60
QY 61 PVICFLMEKCLILYKPNNGDTIGPILVQOQKQKLYISADLVHLIA 106
Db 61 PVICFLMEKCLILYKPNNGDTIGPILVQOQKQKLYISADLVHLIA 106

RESULT 6
ADB37523
ID ADB37523 standard; protein; 106 AA.
XX
AC ADB37523;
XX
XX 04-DEC-2003 (first entry)
XX
DE Neural thread protein-like protein #2.
XX
XX Cytostatic; Antitumour; Antipsoriatic; Dermatological;
KW Antiatherosclerotic; Antiarteriosclerotic; Vasotropic; Antiinflammatory;
KW Immunosuppressive; Tranquillizer; Antiemetic; Virucide; AD7c-NTP;
KW neural thread protein; neuritic sprouting.
XX
OS Unidentified.
XX
XX WO2003008444-A2.
XX
XX 30-JAN-2003.
XX
XX 19-JUL-2002; 2002WO-CA001106.
XX
XX 19-JUL-2001; 2001US-0306150P.
PR 19-JUL-2001; 2001US-0306161P.
PR 16-NOV-2001; 2001US-0331477P.
XX
XX (NYMO-) NYMOX CORP.
XX
XX Averbach PA, Gemmell J;
PI
XX WPI; 2003-248000/24.
XX
XX Novel Related peptide or AD7c-neural thread peptide, useful for treating
PT unwanted cellular proliferations, glandular hyperplasia, unwanted facial
PT hair, warts and unwanted fatty tissue.
XX
XX Disclosure; Fig 5; 109pp; English.
XX
XX The present invention relates to AD7c-neural thread protein (NTP) and
CC related proteins and peptides (I; ADB37528-ADB37641). The sequences are
CC useful for treating a condition in a patient requiring removal or
CC destruction of cells. The condition can be selected from benign or
CC malignant tumour of a tissue, hyperplasia, hypertrophy or overgrowth of a
CC tissue, virally, bacterially or parasitically altered tissue, or
CC malformation of a tissue, where the tissue is selected from lung, breast,
CC stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney, sinus,
CC colon, intestine, stomach, rectum, oesophagus, heart, spleen, salivary
CC gland, blood, brain and its coverings, spinal cord and its coverings,
CC muscle, connective tissue, adrenal, parathyroid, thyroid, uterus, testis,
CC pituitary, reproductive organs, liver, gall bladder, eye, ear, nose,
CC throat, tonsils, mouth, lymph nodes and lymphoid tissue. The condition is
CC preferably consiliary hypertrophy, prostatic hyperplasia, psoriasis,
CC eczema, dermatosis, cosmetic modification to a tissue (skin, eye, ear,
CC nose, throat, mouth, muscle, connective, hair or breast tissue), vascular

CC disease (atherosclerosis or arteriosclerosis), haemorrhoids, varicose
CC veins, inflammatory disease, autoimmune disease, metabolic disease,
CC hereditary/genetic disease, traumatic disease or physical injury,
CC nutritional deficiency disease, infectious disease, amyloid disease,
CC fibrosis disease, storage disease, congenital malformation, enzyme
CC deficiency disease, poisoning, intoxication, environmental disease,
CC radiation disease, endocrine disease, degenerative disease and mechanical
CC disease. The peptides are useful for treating unwanted cellular
CC proliferations, glandular (e.g. prostate) hyperplasia, unwanted facial
CC hair, warts and unwanted fatty tissue, or for preparing antibodies that
CC recognize and/or bind to Related proteins, Related peptides or NTP
CC peptides. The present sequence was used to illustrate the invention.
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 582; DB 7; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.1e-63;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60
Db 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60
QY 61 PVICFLMEKCLILYKPNNGDTIGPILVQOQKQKLYISADLVHLIA 106
Db 61 PVICFLMEKCLILYKPNNGDTIGPILVQOQKQKLYISADLVHLIA 106

RESULT 7
AAO06149
ID AAO06149 standard; protein; 119 AA.
XX
AC AAO06149;
XX
XX 06-NOV-2001 (first entry)
DT
DE Human polypeptide SEQ ID NO 20041.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
XX Homo sapiens.
XX
XX WO200164835-A2.
PN
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US004927.
XX
XX 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Tang YT, Liu C, Drmanac RT;
PI
XX WPI; 2001-514838/56.
DR N-PSDB; AAI86080.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX
XX Claim 20; SEQ ID NO 20041; 1399pp + Sequence Listing; English.
PS
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating

CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 119 AA;
SQ Query Match 40.8%; Score 237.5; DB 4; Length 119;
Best Local Similarity 72.1%; Pred. No. 6.7e-21;
Matches 44; Conservative 4; Mismatches 10; Indels 3; Gaps 1;
QY 12 FFEFESHSLTQAGVQWCELGSQPLPSGFRFSCLSLLSSWDYSHEPPHPV---ICSFLLM 68
DB 2 FFEFESHVAGVQWCDLGLSQPLPLGLKEFSCLSLLSSWDYRHTPPHPANLFFVFSFLV 61
QY 69 E 69
DB 62 E 62
RESULT 8
AAB28760
ID AAB28760 standard; protein; 85 AA.
XX AC AAB28760;
XX DT 30-JAN-2001 (first entry)
XX DE Peptide #5.
XX KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnerable; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX OS Homo sapiens.
XX PN WO200055198-A1.
XX PD 21-SEP-2000.
XX PF 09-MAR-2000; 2000WO-US006012.
XX PR 12-MAR-1999; 99US-0124093P.
XX PR 23-NOV-1999; 99US-0166989P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Ruben SM, Komatsoulis G;
XX DR WPI; 2000-587520/55.
XX PT Human secreted proteins and the nucleic acids that encode them, useful in
XX gene therapy protocols and recombinant nucleic acid based procedures.
XX PS Disclosure; Page 369; 391pp; English.
XX CC Sequences AAB28702-B28751 represent the amino acid sequences of 50 human
CC secreted proteins encoded by the genes AAC59907-C59956. The genes and
CC proteins are useful for preventing, ameliorating or treating medical
CC conditions, e.g. by protein or gene therapy. The genes are isolated from
CC a range of human tissues disclosed in the specification. The nucleic
CC acids, proteins, antibodies and (ant)agonists are useful in the
CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer, and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b)
CC immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing

CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. The present sequence was used in the invention
XX Sequence 85 AA;
SQ Query Match 40.3%; Score 234.5; DB 3; Length 85;
Best Local Similarity 72.1%; Pred. No. 1e-20;
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;
QY 8 FCFEFETESHSLTQAGVQWCELGSQPLPSGFRFSCLSLLSSWDYSHEPPHPV-ICSF 66
DB 7 FNFCLFEMESHSLTQAGVQWPNLGLSQPLPLGLKRFSCLSLPSWDYGHLPHPANFCIF 66
QY 67 L 67
DB 67 I 67
RESULT 9
AAB01399
ID AAB01399 standard; protein; 375 AA.
XX AC AAB01399;
XX DT 20-OCT-2000 (first entry)
XX DE Neuron-associated protein.
XX KW Neuron associated protein; NEUAP; neurological disorder; epilepsy;
KW ischemic cerebrovascular disease; stroke; cerebral neoplasm;
KW Alzheimer's disease; Pick's disease; Huntington's disease; dementia;
KW Parkinson's disease; demyelinating disease; meningitis; prion disease;
KW Kuru; Creutzfeldt-Jakob disease; neurofibromatosis; cerebral palsy;
KW muscular dystrophy; central nervous system; CNS;
KW peripheral nervous system; PNS; myopathy; schizophrenia;
KW atrophic keratosis; arteriosclerosis; atherosclerosis; bursitis;
KW cirrhosis; hepatitis; mixed connective tissue disease; MCTD;
KW myelofibrosis; paroxysmal nocturnal haemoglobinuria; cancer;
KW autoimmune disease; inflammation; acquired immunodeficiency syndrome;
KW AIDS; Addison's disease; adult respiratory distress syndrome; allergy;
KW ankylosing spondylitis; amyloidosis; anaemia; asthma;
KW werner syndrome, trauma; human.
XX OS Homo sapiens.
XX PN WO200034477-A2.
XX PD 15-JUN-2000.
XX PF 10-DEC-1999; 99WO-US030408.
XX PR 11-DEC-1998; 98US-00210083.
XX PR 09-FEB-1999; 99US-0119365P.
XX PR 16-MAR-1999; 99US-0124687P.
XX PA (INCY-) INCYTE PHARM INC.
XX PI Tang YT, Yue H, Baughn MR, Hillman JL, Lal P, Au-Young J;
XX PI Yang J, Lu DAM, Azimzai Y;
XX WPI; 2000-423423/36.
XX DR New human neuron-associated proteins and polynucleotides encoding them,
XX PT useful for diagnosis, treatment and prevention of cell proliferative
XX disorders including cancer, neuronal and neurological disorders.
XX PS Disclosure; Page 143-144; 145pp; English.
XX CC Human neuron-associated proteins (NEUAP) can be used for treating or
CC preventing a disorder associated with decreased expression or activity of
CC NEUAP. Antagonists of NEUAP are useful for treating or preventing
CC disorder associated with increased expression or activity of NEUAP. NEUAP

PT cells, such as a benign or malignant tumor of a tissue or an inflammatory
PT disease, comprises administering a neural thread protein (NTP) or a NTP
XX gene to a mammal.

PS Example 2; Fig 1; 70pp; English.

XX The invention relates to a method for treating a condition in a patient
CC requiring removal or destruction of cells. The method involves
CC administering to a mammal a neural thread protein (NTP), or administering
CC to a tumour or other target cell a NTP gene, where the expression of the
CC NTP gene is induced resulting in expression of the NTP protein. The
CC method and NTP are useful for treating a condition in a patient requiring
CC removal or destruction of cells, such as a benign or malignant tumour of
CC a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue,
CC preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,
CC bacterially, or parasitically altered tissue, or a malformation of a
CC tissue. Other conditions include a cosmetic modification to a tissue,
CC such as removal of unwanted facial hair, warts or unwanted fatty tissue,
CC a vascular disease, particularly atherosclerosis or arteriosclerosis,
CC haemorrhoids, or varicose veins, an inflammatory disease, autoimmune
CC disease, metabolic disease, hereditary/genetic disease, traumatic disease
CC or physical injury, nutritional deficiency disease, infectious disease,
CC congenital malformation, amyloid disease, fibrosis disease, storage
CC disease, enzyme deficiency disease, poisoning, intoxication, degenerative
CC disease, radiation disease, environmental disease, endocrine disease or
CC mechanical disease. The invention is useful in protein therapy and gene
CC therapy. The present sequence is AD7c-NTP protein

XX Sequence 375 AA;

Query Match 40.3%; Score 234.5; DB 5; Length 375;
Best Local Similarity 72.1%; Pred. No. 6.7e-20;
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

Qy 8 FCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPHPV-ICSF 66
Db 297 FNFLCFEMESHVSVTQAGVQWPNLGLSLQPLPGLKRFSCSLSPSSWDYGHLPHPANFCIF 356

Qy 67 L 67
Db 357 I 357

RESULT 12
ABR63268
ID ABR63268 standard; protein; 375 AA.

XX ABR63268;

XX 28-AUG-2003 (first entry)

DE AD7c-NTP protein.

XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour.

XX Unidentified.

PN WO2003008443-A2.

XX 30-JAN-2003.

PF 19-JUL-2002; 2002WO-CA001105.

XX 19-JUL-2001; 2001US-0306150P.

PR 19-JUL-2001; 2001US-0306161P.

XX 16-NOV-2001; 2001US-0331477P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-247999/24.

XX
PT
XX
XX
PS

Novel neural thread protein peptide, referred as cell death peptide,
useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.

Disclosure; Fig 1; 77pp; English.

XX The present invention relates to a neural thread protein (NTP) peptide
CC referred to as cell death peptide. Thought to be cytostatic,
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC treating a condition in a patient requiring removal or destruction of
CC cells, for treating a condition such as benign or malignant tumor,
CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for
CC a pancreatic thread protein. The peptide is conjugated, linked or bound
CC to a molecule chosen from antibody or its fragment, antibody-like binding
CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side
CC effects of surgery. The present sequence is an NTP amino acid sequence

XX Sequence 375 AA;

Query Match 40.3%; Score 234.5; DB 6; Length 375;
Best Local Similarity 72.1%; Pred. No. 6.7e-20;
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

Qy 8 FCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPHPV-ICSF 66
Db 297 FNFLCFEMESHVSVTQAGVQWPNLGLSLQPLPGLKRFSCSLSPSSWDYGHLPHPANFCIF 356

Qy 67 L 67
Db 357 I 357

RESULT 13
ADA84017
ID ADA84017 standard; protein; 375 AA.

XX ADA84017;

XX 20-NOV-2003 (first entry)

XX Human POM80 protein.

XX human; marker; expressed sequence tag; EST; arabidopsis; tumour;

KW stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;

KW vaccine.

XX Homo sapiens.

XX WO2002103028-A2.

XX 27-DEC-2002.

XX 30-MAY-2002; 2002WO-IB004189.

XX 30-MAY-2001; 2001US-0293999P.

PR 22-OCT-2001; 2001US-0330457P.

PR 19-FEB-2002; 2002US-0357144P.

XX (BIOM-) BIOMEDICAL CENT.

XX Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;

XX WPI; 2003-175241/17.

DR N-PSDB; ADA84016.

XX Determining if a nucleic acid is a marker for a phenotype/cell type of
PT interest, by global comparison of expressed sequence tags known to be
PT expressed in the phenotype/cell type with all ESTs expressed in normal
PT tissue.

XX Claim 29; Page 398-400; 516pp; English.

XX The invention relates to a novel method for determining if a nucleic acid

CC is a marker for a predetermined phenotype/cell type of interest from a

CC biological species. The method comprises performing a global comparison

CC of a group of expressed sequence tags (ESTs) known to be expressed in the

CC phenotype/cell type of interest with all ESTs expressed in normal tissue

CC in order to identify ESTs that are preferentially expressed in the

CC phenotype/cell of interest. A method of the invention is useful for

CC determining whether a nucleic acid is a marker for a predetermined

CC phenotype or cell type of interest from a biological species, preferably

CC Arabidopsis or human. The cell type of interest is an abnormal cell such

CC as a tumour cell, and the predetermined phenotype is a stress-induced

CC phenotype such as hypersensitive stress or high salt conditions. A method

CC of the invention is also useful for determining the progression of colon

CC cancer in a human, for detecting a tumour cell, and for regulating or

CC preventing the growth of a tumour cell. An antibody of the invention is

CC useful for detecting the absence or presence of peptides encoded by

CC tumour-associated markers. A polypeptide of the invention is useful as an

CC immunogen for vaccinating an animal. The present sequence represents a

CC tumour-associated antigen of the invention.

XX Sequence 375 AA;

CC Query Match 40.3%; Score 234.5; DB 6; Length 375;

CC Best Local Similarity 72.1%; Pred. No. 6.7e-20;

CC Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

QY 8 FCFCFFETESHSLTQAGVQWVCELGSPQLPSGFKRFSCLLSGWDYSHPPHPV-ICSF 66

Db 297 FNFCLFEMESHVSTQAGVQWVNLGSLQPLPGLKRFSLCLSLPSSWDYGHLPHPANFCIF 356

QY 67 L 67

Db 357 I 357

RESULT 14

ID ABU03024 standard; protein; 375 AA.

XX ABU03024;

AC ABU03024;

XX 20-JAN-2003 (first entry)

XX Human neural thread protein AD7C-NTP.

XX Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;

KW transplantation; grafting; chemotherapy; immunotherapy; vaccination;

KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;

KW radiation; tumour; hyperplasia; hypertrophy; overgrowth of tissue;

KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;

KW cosmetic modification; vascular disease; atherosclerosis;

KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;

KW autoimmune disease; metabolic disease; traumatic disease;

KW physical injury; nutritional deficiency disease; infectious disease;

KW amyloid disease; fibrosis disease; storage disease;

KW congenital malformation; enzyme deficiency disease; poisoning;

KW intoxication; environmental disease; radiation disease;

KW endocrine disease; degenerative disease; mechanical disease.

XX Homo sapiens.

XX W0200297030-A2.

XX 05-DEC-2002.

XX 24-MAY-2002; 2002WO-CA000759.

XX 25-MAY-2001; 2001US-0293156P.

XX (NYMO-) NYMOX CORP.

XX Averback PA;

XX WPI; 2003-041406/03.

XX Novel peptides similar in amino acid sequence to neural thread proteins

PT (NTP), useful for treating unwanted cellular proliferations such as

PT malignant tumors and prostatic hyperplasia.

XX Disclosure; Fig 1; 78pp; English.

XX The invention describes an NTP-peptide (I) comprising at least one amino

CC acid sequence corresponding to part of the amino acid sequence of a

CC neural thread protein, AD7C-NTP. The invention provides a method of

CC treating a condition requiring removal or destruction of cells of a

CC mammal comprising administering to a mammal, a therapeutic amount of (I).

CC The treatment is administered to the mammal before, during or after

CC surgical excision, transplantation, grafting, chemotherapy,

CC immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,

CC laser therapy, phototherapy, gene therapy and/or radiation. The method is

CC useful for treatment of benign or malignant tumour; hyperplasia,

CC hypertrophy or overgrowth of tissue; virally, bacterially or

CC parasitically altered tissue; malformation of tissue selected from lung,

CC breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,

CC sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary

CC gland, blood, brain and its coverings, spinal cord, muscle, connective

CC tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary,

CC reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,

CC tonsils, mouth and lymph nodes and lymphoid system; tonsillary

CC hypertrophy; prostatic hyperplasia; cosmetic modification to a tissue;

CC vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;

CC varicose veins; inflammatory disease; autoimmune disease; metabolic

CC disease; hereditary/genetic disease; traumatic disease; physical injury;

CC nutritional deficiency disease; infectious disease; amyloid disease;

CC fibrosis disease; storage disease; congenital malformation; enzyme

CC deficiency disease; poisoning; intoxication; environmental disease;

CC radiation disease; endocrine disease; degenerative disease and mechanical

CC disease. This is the amino acid sequence of the human neural thread

CC protein AD7C-NTP

XX Sequence 375 AA;

QY 8 FCFCFFETESHSLTQAGVQWVCELGSPQLPSGFKRFSCLLSGWDYSHPPHPV-ICSF 66

Db 297 FNFCLFEMESHVSTQAGVQWVNLGSLQPLPGLKRFSLCLSLPSSWDYGHLPHPANFCIF 356

QY 67 L 67

Db 357 I 357

RESULT 15

ID ABB99774 standard; protein; 375 AA.

XX ABB99774;

AC ABB99774;

XX 24-MAR-2003 (first entry)

XX Amino acid sequence of human neuronal thread protein AD7c-NTP.

XX Human; neuronal thread protein; AD7c-NTP; Alzheimer's disease; histone;

KW neurodegeneration; in vivo gene expression; amphipathic compound;

KW gene therapy.

XX Homo sapiens.

XX W0200299036-A2.

XX

PD		12-DEC-2002.	
XX			
XX		28-MAY-2002; 2002WO-US016429.	
XX			
FR		01-JUN-2001; 2001US-00872968.	
XX		(RHOD-) RHODE ISLAND HOSPITAL.	
PA			
XX			
FI		Wands JR, De La Monte SM;	
XX			
XX		WPI; 2003-140605/13.	
DR		N-PSDB; ABZ23236.	
DR			
XX			
PT		Inducing prolonged in vivo gene expression in mammal by contacting	
FT		neural tissue with composition comprising Alzheimer's disease-	
PT		associated neural thread protein 7c antisense nucleic acid, histone,	
PT		amphipathic compound.	
XX			
PS		Disclosure; Page 35; 69pp; English.	
XX			
CC		The present sequence represents a human neuronal thread protein AD7c-NTP.	
CC		AD7c-NTP is overexpressed in brains with Alzheimer's disease at early and	
CC		intermediate stages of neurodegeneration. The expression of AD7c-NTP may	
CC		be reduced using the method of the invention. The specification describes	
CC		a method for inducing prolonged in vivo gene expression in a mammal. The	
CC		method comprises contacting a non-muscular tissue with a composition	
CC		comprising a nucleic acid, histone and an amphipathic compound. The	
CC		method is useful for inducing prolonged in vivo gene expression in non-	
CC		muscular tissue of a mammal, e.g. neuronal tissue, central nervous system	
CC		(CNS) tissue, tissue comprising a post-mitotic neuronal cell, cortical	
CC		neuronal cell or hippocampal neuronal cell, glial cell, or vascular	
CC		endothelial cell. The method is useful in gene therapy applications to	
CC		treat Alzheimer's disease , where the composition comprises antisense	
CC		AD7c-NTP nucleic acid	
XX			
SQ		Sequence 375 AA;	
	Query Match	40.3%; Score 234.5; DB 6; Length 375;	
	Best Local Similarity	72.1%; Pred. No. 6.7e-20;	
	Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;		
Qy	8 FCFCFFTEHSLTQAGVQMCELGSPPLPGSKRFRCSCLSLLSWDYSHEPPHV-ICSF 66		
Dd	297 FNFCLEWESHSVTQAGVQMNGLSGLQLPPLGKLRFRCSCLSLFSSWDYGHLPHPANPCIF 356		
Qy	67 L 67		
Dd	357 I 357		

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OM protein - protein search, using sw model

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(without alignments)
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Perfect score: 582

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Maximum DB seq length: 2000000000

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Maximum Match 100%

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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	582	100.0	106	14	US-10-146-130-6
3	582	100.0	106	14	US-10-092-934-5
4	582	100.0	106	14	US-10-153-334-5
5	582	100.0	106	14	US-10-198-069-5
6	582	100.0	106	14	US-10-198-070-5
7	234.5	40.3	375	9	US-09-964-666-2
8	234.5	40.3	375	9	US-09-964-412-2
9	234.5	40.3	375	10	US-09-964-667-2
10	234.5	40.3	375	10	US-09-872-368-2
11	234.5	40.3	375	10	US-09-964-678A-2

12	234.5	40.3	375	14	US-10-146-130-2	Sequence 2, Appli
13	234.5	40.3	375	14	US-10-092-934-10	Sequence 10, Appli
14	234.5	40.3	375	14	US-10-153-334-1	Sequence 1, Appli
15	234.5	40.3	375	14	US-10-198-069-1	Sequence 1, Appli
16	234.5	40.3	375	14	US-10-157-031-299	Sequence 299, App
17	234.5	40.3	375	14	US-10-198-070-1	Sequence 1, Appli
18	234.5	40.3	375	16	US-10-755-889-410	Sequence 410, App
19	234.5	40.3	375	17	US-10-910-173-2	Sequence 2, Appli
20	230.5	39.6	89	18	US-10-450-763-40159	Sequence 40159, A
21	230.5	39.6	123	15	US-10-104-047-2112	Sequence 2112, Ap
22	226	38.8	97	15	US-10-276-774-2008	Sequence 2008, Ap
23	223.5	38.4	100	15	US-10-094-749-3044	Sequence 3044, Ap
24	218.5	37.5	101	15	US-10-094-749-2181	Sequence 2181, Ap
25	215.5	37.0	146	18	US-10-450-763-38554	Sequence 38554, A
26	215.5	37.0	433	14	US-10-017-161-2092	Sequence 2092, Ap
27	215.5	37.0	433	15	US-10-292-798-1738	Sequence 1738, Ap
28	214.5	36.9	114	15	US-10-104-047-2423	Sequence 2423, Ap
29	213	36.6	132	18	US-10-450-763-38641	Sequence 38641, A
30	212.5	36.5	93	10	US-09-764-891-5337	Sequence 5337, Ap
31	212.5	36.5	93	14	US-10-205-428-486	Sequence 486, App
32	211	36.3	133	15	US-10-094-749-1865	Sequence 1865, Ap
33	208	35.7	168	18	US-10-450-763-37987	Sequence 37987, A
34	207.5	35.7	91	15	US-10-291-172-264	Sequence 264, App
35	207.5	35.7	91	15	US-10-221-278-264	Sequence 264, App
36	207.5	35.7	129	15	US-10-104-047-2565	Sequence 2565, Ap
37	203.5	35.0	116	13	US-10-001-835-161	Sequence 161, App
38	203	34.9	151	14	US-10-198-070-22	Sequence 22, Appli
39	201	34.5	135	15	US-10-424-599-24280	Sequence 24280, A
40	201	34.5	158	15	US-10-104-047-3047	Sequence 3047, Ap
41	199.5	34.3	105	15	US-10-108-260A-3988	Sequence 3988, Ap
42	199	34.2	127	15	US-10-108-260A-2558	Sequence 2558, Ap
43	198	34.0	62	15	US-10-001-885-98	Sequence 98, Appli
44	198	34.0	62	20	US-11-057-447-98	Sequence 98, Appli
45	198	34.0	74	15	US-10-276-774-1929	Sequence 1929, Ap

ALIGNMENTS

RESULT 1
US-10-138-516-4
; Sequence 4, Application US/10138516
; Publication No. US20030003445A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING ANTIBODIES TO
; TITLE OF INVENTION: NEURAL THREAD PROTEINS
; FILE REFERENCE: 59003.000004
; CURRENT APPLICATION NUMBER: US/10/138.516
; CURRENT FILING DATE: 2002-07-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-516-4

Query Match 100.0%; Score 582; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFFVLYRFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLLSWDSYSHPEPH 60
Db 1 MFFVLYRFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLLSWDSYSHPEPH 60

Qy 61 PVICSLMEKCLILYKNGDTIGPILVQOGRKQKLYISADLVHLIA 106
Db 61 PVICSLMEKCLILYKNGDTIGPILVQOGRKQKLYISADLVHLIA 106

RESULT 2
US-10-146-130-6

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; Sequence 6, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; TITLE OF INVENTION: NEURAL THREAD PROTEINS
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146.130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-6

Query Match      100.0%; Score 582; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60
Db 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60

Qy 61 PVICFLMEKCLILYKPNGTIGPILVQOGKROKLYISADLVHLIA 106
Db 61 PVICFLMEKCLILYKPNGTIGPILVQOGKROKLYISADLVHLIA 106

RESULT 3
US-10-092-934-5
; Sequence 5, Application US/10092934
; Publication No. US20030054990A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHODS OF USING NEURAL THREAD PROTEINS TO TREAT TUMORS
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018792-0199
; CURRENT APPLICATION NUMBER: US/10/092.934
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/273,957
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-934-5

Query Match      100.0%; Score 582; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60
Db 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60

Qy 61 PVICFLMEKCLILYKPNGTIGPILVQOGKROKLYISADLVHLIA 106
Db 61 PVICFLMEKCLILYKPNGTIGPILVQOGKROKLYISADLVHLIA 106

RESULT 4
US-10-153-334-5
; Sequence 5, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
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; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003-000006
; CURRENT APPLICATION NUMBER: US/10/153.334
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,156
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-334-5

Query Match      100.0%; Score 582; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60
Db 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60

Qy 61 PVICFLMEKCLILYKPNGTIGPILVQOGKROKLYISADLVHLIA 106
Db 61 PVICFLMEKCLILYKPNGTIGPILVQOGKROKLYISADLVHLIA 106

RESULT 5
US-10-198-069-5
; Sequence 5, Application US/10198069
; Publication No. US20030096756A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000009
; CURRENT APPLICATION NUMBER: US/10/198.069
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-069-5

Query Match      100.0%; Score 582; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60
Db 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60

Qy 61 PVICFLMEKCLILYKPNGTIGPILVQOGKROKLYISADLVHLIA 106
Db 61 PVICFLMEKCLILYKPNGTIGPILVQOGKROKLYISADLVHLIA 106

RESULT 6
US-10-198-070-5
; Sequence 5, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMELL, JACK
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;; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
;; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
;; TITLE OF INVENTION: CELLS
;; FILE REFERENCE: 59003.000008
;; CURRENT APPLICATION NUMBER: US/10/198.070
;; CURRENT FILING DATE: 2002-07-19
;; PRIOR APPLICATION NUMBER: 60/306,161
;; PRIOR FILING DATE: 2001-07-19
;; PRIOR APPLICATION NUMBER: 60/306,150
;; PRIOR FILING DATE: 2001-07-19
;; PRIOR APPLICATION NUMBER: 60/331,477
;; PRIOR FILING DATE: 2001-11-16
;; NUMBER OF SEQ ID NOS: 125
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 5
;; LENGTH: 106
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-198-070-5

Query Match 100.0%; Score 582; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFFVLYRFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLLSLSSWDYSHEPPH 60
Db 1 MFFVLYRFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLLSLSSWDYSHEPPH 60
Qy 61 PVICSLMEKCLILYKNGDTIGPILVQOGRKQKLYISADLVHIA 106
Db 61 PVICSLMEKCLILYKNGDTIGPILVQOGRKQKLYISADLVHIA 106

RESULT 7

US-09-964-666-2
; Sequence 2, Application US/09964666
; Patent No. US20020104108A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; Wands, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention
; of Alzheimer's Disease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/964,666
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0609.4370000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-964-666-2

Query Match 40.3%; Score 234.5; DB 9; Length 375;
Best Local Similarity 72.1%; Pred. No. 2.1e-18;
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;
Qy 8 FCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLLSLSSWDYSHEPPHVC-ICSF 66
Db 297 FNCLFEMESHVQTQAGVQWPNLGSLOPLPGLKRFCSCLSLPSSWDYGHLPHPANFCIF 356
Qy 67 L 67
Db 357 I 357

RESULT 8

US-09-964-412-2
; Sequence 2, Application US/09964412
; Patent No. US20020129391A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; Wands, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention
; of Alzheimer's Disease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/964,412
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0609.4370000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-964-412-2

Query Match 40.3%; Score 234.5; DB 9; Length 375;
Best Local Similarity 72.1%; Pred. No. 2.1e-18;
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;
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Db 297 FNCLFEMESHVQTQAGVQWPNLGSLOPLPGLKRFCSCLSLPSSWDYGHLPHPANFCIF 356
Qy 67 L 67
Db 357 I 357

RESULT 9

US-09-964-667-2
; Sequence 2, Application US/09964667
; Publication No. US20030033621A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; Wands, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention
; of Alzheimer's Disease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/964,667
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0609.4370000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-964-667-2

Query Match 40.3%; Score 234.5; DB 10; Length 375;
Best Local Similarity 72.1%; Pred. No. 2.1e-18;
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;
QY 8 FCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHPEPPHPV-ICSF 66
Db 297 FNFCLFEMESHVQTQAGVQWPNLGSLOPLPPGLKRFSCSLPSWDYGHLPHPANFCIF 356
QY 67 L 67
Db 357 I 357

RESULT 10
US-09-872-968-2
; Sequence 2, Application US/09872968
; Publication No. US20030050262A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R
; APPLICANT: de la Monte, Suzanne M
; TITLE OF INVENTION: Inhibition of Neurodegeneration
; FILE REFERENCE: 21486-047
; CURRENT APPLICATION NUMBER: US/09/872,968
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-968-2

Query Match 40.3%; Score 234.5; DB 10; Length 375;
Best Local Similarity 72.1%; Pred. No. 2.1e-18;
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

QY 8 FCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHPEPPHPV-ICSF 66
Db 297 FNFCLFEMESHVQTQAGVQWPNLGSLOPLPPGLKRFSCSLPSWDYGHLPHPANFCIF 356
QY 67 L 67
Db 357 I 357

RESULT 11
US-09-964-678A-2
; Sequence 2, Application US/09964678A
; Publication No. US20030066097A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs
; TITLE OF INVENTION: Effective for the Treatment or Prevention of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 0609.4370002
; CURRENT APPLICATION NUMBER: US/09/964,678A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 09/380,203
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US98/03685
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/038,908
; PRIOR FILING DATE: 1997-02-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: AD7c-NTP cDNA
US-09-964-678A-2

Query Match 40.3%; Score 234.5; DB 10; Length 375;
Best Local Similarity 72.1%; Pred. No. 2.1e-18;
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;
QY 8 FCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHPEPPHPV-ICSF 66
Db 297 FNFCLFEMESHVQTQAGVQWPNLGSLOPLPPGLKRFSCSLPSWDYGHLPHPANFCIF 356
QY 67 L 67
Db 357 I 357

RESULT 12
US-10-146-130-2
; Sequence 2, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 40.3%; Score 234.5; DB 14; Length 375;

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Job time : 178.706 secs

Query Match 40.3%; Score 234.5; DB 14; Length 375;

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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:19 ; Search time 24.2326 Seconds
(without alignments)
326.535 Million cell updates/sec

Title: US-10-092-934-5

Perfect score: 582

Sequence: 1 MFFVLRFPCFETESHSL.....VQGGKQKLYISADLVHLIA 106

Scoring table: BLOSUM62

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
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 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	234.5	40.3	375	2	US-08-454-557C-121
2	234.5	40.3	375	2	US-08-340-426D-121
3	234.5	40.3	375	2	US-08-450-673C-121
4	234.5	40.3	375	4	US-09-872-968-2
5	214	36.8	397	5	PCT-US95-1711A-121
6	206	35.4	61	4	US-09-513-999C-4581
7	194.5	33.4	87	4	US-09-205-258-342
8	194.5	33.4	119	4	US-09-513-999C-7867
9	184	31.6	60	4	US-09-513-999C-7075
10	184	31.6	87	4	US-09-621-976-5968
11	182	31.3	96	4	US-09-513-999C-6065
12	182	31.3	102	4	US-09-621-976-6112
13	181.5	31.2	97	4	US-09-513-999C-4770
14	180.5	31.0	66	4	US-09-621-976-5606
15	180	30.9	60	4	US-09-513-999C-7143
16	179	30.8	87	4	US-09-621-976-4482
17	179	30.8	121	4	US-09-513-999C-7874
18	174	29.9	108	4	US-09-513-999C-7878
19	172.5	29.6	64	4	US-09-621-976-5588
20	172	29.6	54	4	US-09-513-999C-7519
21	172	29.6	76	4	US-09-621-976-6338
22	170	29.2	58	4	US-09-513-999C-4523
23	170	29.2	59	4	US-09-471-276-1317
24	168	28.9	65	4	US-09-513-999C-6665
25	168	28.9	92	4	US-09-248-796A-16335
26	166	28.5	90	4	US-09-621-976-4397
27	165	28.4	70	4	US-09-513-999C-6561

28	164.5	28.3	132	4	US-09-636-215-573	Sequence 573, App
29	164.5	28.3	132	4	US-09-685-166A-573	Sequence 573, App
30	164.5	28.3	132	4	US-09-679-143-573	Sequence 573, App
31	164.5	28.3	132	4	US-09-651-236-573	Sequence 573, App
32	164.5	28.3	132	4	US-09-685-166A-884	Sequence 884, App
33	164.5	28.3	135	4	US-09-679-426-884	Sequence 884, App
34	164.5	28.3	135	4	US-09-759-143-884	Sequence 884, App
35	164.5	28.3	135	4	US-09-621-976-5929	Sequence 5929, App
36	160	27.5	91	4	US-09-621-976-6005	Sequence 6005, App
37	159	27.3	63	4	US-09-513-999C-5327	Sequence 5327, App
38	158.5	27.2	776	4	US-10-020-079-24	Sequence 24, App1
39	158.5	27.2	789	4	US-10-020-079-22	Sequence 22, App1
40	158.5	27.2	863	4	US-10-020-079-32	Sequence 32, App1
41	158.5	27.2	863	4	US-10-020-079-30	Sequence 30, App1
42	158.5	27.2	889	4	US-10-020-079-20	Sequence 20, App1
43	158.5	27.2	895	4	US-10-020-079-18	Sequence 18, App1
44	158.5	27.2	895	4	US-10-020-079-28	Sequence 28, App1
45	158.5	27.2	976	4	US-10-020-079-28	Sequence 28, App1

ALIGNMENTS

RESULT 1

US-08-454-557C-121

; Sequence 121, Application US/08454557C

; Patent No. 5830670

; GENERAL INFORMATION:

; APPLICANT: de la Monte, Suzanne

; APPLICANT: Wands, Jack R.

; TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection

; NUMBER OF SEQUENCES: 121

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

; STREET: 1100 New York Avenue, Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/454,557C

; FILING DATE: 30-MAY-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Ludwig, Steven R.

; REGISTRATION NUMBER: 36,203

; REFERENCE/DOCKET NUMBER: 0609.3840003

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 121:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 375 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-454-557C-121

Query Match 40.3%; Score 234.5; DB 2; Length 375;

Best Local Similarity 72.1%; Pred. No. 3.3e-21;

Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

Qy 8 FCFCFFETESHSLTOAGVOWCELGSPDLPSCGFKRFSCLLSLSSWDYSHEPHPV-ICSF 66

Db 297 FNFCLFEMESHVSVTQAGVQWPNLGLSLOPLPGLKRFSCLLSLOPSSWDYGHLPHPANFCIF 356

Qy 67 L 67

Db 357 I 357

RESULT 2

US-08-340-426D-121

Sequence 121, Application US/08340426D

Patent No. 5948634

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

APPLICANT: Wands, Jack R.

TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection

TITLE OF INVENTION: of Alzheimer's Disease

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/340,426D

FILING DATE: 14-NOV-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0609.3840002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 121:

SEQUENCE CHARACTERISTICS:

LENGTH: 375 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-340-426D-121

Query Match 40.3%; Score 234.5; DB 2; Length 375;

Best Local Similarity 72.1%; Pred. No. 3.3e-21;

Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

QY 8 FCFCFFETESHSLTQAGVQWVCELGSPQLPSGFKRFSCLSLSSWDYSHEPPHPV-ICSP 66

Db 297 FNFCLFEMESHVSQTQGVQWPNLGLSLQPLPGLKRFSCSLSPSSWDYGHLPHPANFCIF 356

QY 67 L 67

Db 357 I 357

RESULT 3

US-08-450-673C-121

Sequence 121, Application US/08450673C

Patent No. 5948888

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

APPLICANT: Wands, Jack R.

TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection

TITLE OF INVENTION: of Alzheimer's Disease

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,673C

FILING DATE: 30-MAY-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0609.3840004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 121:

SEQUENCE CHARACTERISTICS:

LENGTH: 375 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-450-673C-121

Query Match 40.3%; Score 234.5; DB 4; Length 375;

Best Local Similarity 72.1%; Pred. No. 3.3e-21;

Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

QY 8 FCFCFFETESHSLTQAGVQWVCELGSPQLPSGFKRFSCLSLSSWDYSHEPPHPV-ICSP 66

Db 297 FNFCLFEMESHVSQTQGVQWPNLGLSLQPLPGLKRFSCSLSPSSWDYGHLPHPANFCIF 356

QY 67 L 67

Db 357 I 357

RESULT 4

US-09-872-968-2

Sequence 2, Application US/09872968

Patent No. 6770797

GENERAL INFORMATION:

APPLICANT: Wands, Jack R

APPLICANT: de la Monte, Suzanne M

TITLE OF INVENTION: Inhibition of Neurodegeneration

FILE REFERENCE: 21486-047

CURRENT APPLICATION NUMBER: US/09/872,968

CURRENT FILING DATE: 2001-06-01

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 2

LENGTH: 375

TYPE: PRT

ORGANISM: Homo sapiens

US-09-872-968-2

Query Match 40.3%; Score 234.5; DB 4; Length 375;

Best Local Similarity 72.1%; Pred. No. 3.3e-21;

Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

QY 8 FCFCFFETESHSLTQAGVQWVCELGSPQLPSGFKRFSCLSLSSWDYSHEPPHPV-ICSP 66

Db 297 FNFCLFEMESHVSQTQGVQWPNLGLSLQPLPGLKRFSCSLSPSSWDYGHLPHPANFCIF 356

QY 67 L 67

Db 357 I 357

RESULT 5

PCT-US95-17111A-121

; Sequence 121, Application PC/TUS9517111A
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
; TITLE OF INVENTION: Detection of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17111A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,426
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-17111A-121

Query Match 36.8%; Score 214; DB 5; Length 397;
Best Local Similarity 67.7%; Pred. No. 1.4e-18;
Matches 42; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

Qy 8 FCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPHVICSEFL 67
Db 298 FNCLFEMESHVSQTQAGVQWPNLGLQPLPGLKRFKFSCLSLPSSWDYGHLLHHTPLIFVFS 357

Qy 68 ME 69

Db 358 LE 359

RESULT 6
US-09-513-999C-4581
; Sequence 4581, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4581
; LENGTH: 61

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -16...-1
; OTHER INFORMATION: score 7.5
; OTHER INFORMATION: seq LFCLSVCLFEVES/HS
US-09-513-999C-4581

Query Match 35.4%; Score 206; DB 4; Length 61;
Best Local Similarity 69.6%; Pred. No. 1.3e-18;
Matches 39; Conservative 1; Mismatches 14; Indels 2; Gaps 1;

Qy 8 PCF--CFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPHP 61
Db 5 FCLSVCLFEVESHSVTQAGVQWHLGLPLNLPFGKRFKFSCLSLSSWDYRHAPPPP 60

RESULT 7
US-09-205-258-342
; Sequence 342, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 342
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (87)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-342

Query Match 33.4%; Score 194.5; DB 4; Length 87;
Best Local Similarity 61.2%; Pred. No. 5.9e-17;
Matches 41; Conservative 4; Mismatches 17; Indels 5; Gaps 3;

QY 8 FC---FCF-PETESHSLTQAGVQWCELGSPQLPSPGKRFSCLSLLSSWDYSHEPPHV- 62
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 4 FCFVLCFVEMSSSVTQAGVQWCDLGSLLQAPPSPGSPFSCLSLSSWDYRRPPRPN 63
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 63 ICFLME 69
| | | | |
Db 64 FLYFLVE 70
| | | | |

RESULT 8
US-09-513-999C-7867
; Sequence 7867, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-342

Query Match 33.4%; Score 194.5; DB 4; Length 87;
Best Local Similarity 61.2%; Pred. No. 5.9e-17;
Matches 41; Conservative 4; Mismatches 17; Indels 5; Gaps 3;

QY 8 FC---FCF-PETESHSLTQAGVQWCELGSPQLPSPGKRFSCLSLLSSWDYSHEPPHV- 62
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 4 FCFVLCFVEMSSSVTQAGVQWCDLGSLLQAPPSPGSPFSCLSLSSWDYRRPPRPN 63
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 63 ICFLME 69
| | | | |
Db 64 FLYFLVE 70
| | | | |

RESULT 8
US-09-513-999C-7867
; Sequence 7867, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7867
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -16..-1
; OTHER INFORMATION: score 6.5
; OTHER INFORMATION: seq VLXLVCLFETES/XS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: -11
; OTHER INFORMATION: Xaa=Phe or His or Leu or Tyr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 1
; OTHER INFORMATION: Xaa=Gly or Arg
US-09-513-999C-7867

Query Match 33.4%; Score 194.5; DB 4; Length 119;
Best Local Similarity 67.8%; Pred. No. 8.8e-17;
Matches 40; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

QY 1 MFFVLVRFCCFPETESHSLTQAGVQWCELGSPQLPSPGKRFSCLSLLSSWDYSHEPP 59
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 MIFVLXLF-VCLFETESXSVARAGVQWHLVLSURLPPGPFKRFSCLSLLSSWDYRRVPP 58
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 9
US-09-513-999C-7075
; Sequence 7075, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7075
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-7075

Query Match 31.6%; Score 184; DB 4; Length 60;
Best Local Similarity 60.3%; Pred. No. 7.9e-16;
Matches 35; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 2 FVFLVRFCCFPETESHSLTQAGVQWCELGSPQLPSPGKRFSCLSLLSSWDYSHEPP 59
: : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 3 YIYIVFLFYFFFMNSCCFQAQGVQWRDLGSLQPPSPGFKQFSCLSLLSSWDYRRHPP 60
: : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 10
US-09-621-976-5968
; Sequence 5968, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

```

; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5968
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-5968

Query Match 31.6%; Score 184; DB 4; Length 87;
Best Local Similarity 52.7%; Pred. No. 1.3e-15;
Matches 39; Conservative 5; Mismatches 18; Indels 12; Gaps 2;

Qy 12 FFETESHSLTOAGVQWCELGSQPPLPSGFKRFSCLSLSSWDYSHPPHPV-ICSFLEMEK 70
Db 24 FFETFCVAEAKVWCDLGSLOPLLPGRFKRFSCHLSLSSWDCRHLPPHQANFCIF---- 79

Qy 71 CLILYKPNGDTIGP 84
Db 80 -----SGDGVSP 86

RESULT 11
US-09-513-999C-6065
; Sequence 6065, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59. US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6065
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6065

Query Match 31.3%; Score 182; DB 4; Length 96;
Best Local Similarity 60.0%; Pred. No. 2.6e-15;
Matches 36; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Qy 20 LTQAGVQWCELGSQPPLPSGFKRFSCLSLSSWDYSHPPHPVICSFLEMEKCLILYKPNG 79
Db 6 VAQAGVQWRDLGSGPQLPPGPKRFSCLFSLPSSWDYRHVPLLPANLVFLVENGFLHVGPGAG 65

RESULT 12
US-09-621-976-6112
; Sequence 6112, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6112
; LENGTH: 102
; TYPE: PRT

; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5968
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6112

Query Match 31.3%; Score 182; DB 4; Length 102;
Best Local Similarity 59.0%; Pred. No. 2.8e-15;
Matches 36; Conservative 6; Mismatches 17; Indels 2; Gaps 2;

Qy 7 RFCFCFFETESHSLTOAGVQWCELGSQPPLPSGFKRFSCLSLSSWDYSHPPHPV-ICS 65
Db 32 KICL-FFETEAHCVALAXVQWRDIGSLQPLPLGLKQSSCLSLSSWDYRLPLPPHPANFCI 90

Qy 66 F 66
Db 91 F 91

RESULT 13
US-09-513-999C-4770
; Sequence 4770, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59. US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4770
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 8
; OTHER INFORMATION: Xaa=Ala or Glu or Gly or Val
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 82
; OTHER INFORMATION: Xaa=Ala or Pro
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 94
; OTHER INFORMATION: Xaa=Asn or Thr
US-09-513-999C-4770

Query Match 31.2%; Score 181.5; DB 4; Length 97;
Best Local Similarity 45.6%; Pred. No. 3e-15;
Matches 41; Conservative 8; Mismatches 24; Indels 17; Gaps 3;

Qy 1 MFFVL-----YRFCFCFFETESHSLTOAGVQWCELGSQPPLPSGFKRFSCLSLSSWDYS 55
Db 1 MSFILINXVPFLFLFIYFETGSHFTVQAGGKMRGLSLQPLPPGFRSSCLSLSSGWDGCG 60

Qy 56 HEPPHPV-ICSFLEMEKCLILYKPNGDTIGP 84
Db 61 LAPPSANFCIF-----SGDGVSP 79

RESULT 14
US-09-621-976-5606
; Sequence 5606, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
```

Search completed: October 11, 2005, 07:42:49
Job time : 24.2326 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 15.1979 Seconds
(without alignments)
620.432 Million cell updates/sec

Title: US-10-092-934-6
Perfect score: 531
Sequence: 1 EAYTMLHLPTNRPKIAHC.....SRTSNSTPTNSFLWTSSKPR 98

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	16.6	400	2 S58222	PQ-rich protein -
2	82	15.4	215	2 T45846	zinc-finger-like p
3	81	15.3	340	1 WMBEL1	latency-related pr
4	80.5	15.2	365	2 T15478	hypothetical prote
5	80.5	15.2	670	1 S50591	myb-related protei
6	79.5	15.0	239	2 B86346	F16F4.1 protein -
7	79	14.9	1173	2 I50620	prockr2 - chicken
8	77.5	14.6	728	2 T43632	serine/threonine p
9	77.5	14.6	792	2 T43630	serine/threonine p
10	77.5	14.6	1080	2 T27622	hypothetical prote
11	77.5	14.6	7576	2 T17428	FK506 polyketide s
12	77	14.5	437	2 S18407	acrosin (EC 3.4.21
13	76.5	14.4	257	2 T03136	hypothetical prote
14	76.5	14.4	258	2 T51689	probable transcrip
15	76.5	14.4	365	2 D86470	F21H2.9 protein -
16	76.5	14.4	1370	2 T19188	hypothetical prote
17	75.5	14.2	6420	2 T30283	polyketide synthas
18	75	14.1	317	2 D72700	hypothetical prote
19	75	14.1	639	2 T13151	adaptor protein CM
20	74	13.9	323	2 T06506	glutenin low molec
21	74	13.9	374	2 T37676	zinc-finger protei
22	74	13.9	671	2 S51599	Om(2D) protein - f
23	74	13.9	733	2 S44876	ZC21.4 protein - C
24	74	13.9	859	2 S64195	HRR1 protein - yea
25	74	13.9	1093	1 S50614	regulatory protein B
26	73.5	13.8	640	2 A41726	homeotic protein B
27	73.5	13.8	642	2 T27806	homeotic protein B
28	73.5	13.8	1221	2 T13283	probable transcrip
29	73	13.7	1013	2 G71460	probable outer mem

30	72.5	13.7	628	2 S01955	hypothetical prote
31	72.5	13.7	628	2 S19150	hypothetical prote
32	72.5	13.7	1043	2 T13172	gag-like protein p
33	72	13.6	1029	2 S64731	serine/threonine-s
34	71.5	13.5	493	2 A34220	homeotic protein A
35	71	13.4	318	2 T33874	hypothetical prote
36	71	13.4	668	2 S39836	hypothetical prote
37	70.5	13.3	435	2 T30114	hypothetical prote
38	70	13.2	121	2 G82853	hypothetical prote
39	70	13.2	230	2 T28284	hypothetical prote
40	70	13.2	491	2 A32584	Abd-B protein - fr
41	70	13.2	525	1 S39834	myb-related protei
42	70	13.2	544	2 S15664	transcription fact
43	70	13.2	548	2 S52735	CW17R protein - mo
44	70	13.2	901	2 S50987	SOK1 protein - yea
45	70	13.2	1061	2 JC7116	xsal-3 protein - A

ALIGNMENTS

RESULT 1

S58222
PQ-rich protein - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C:Accession: S58222
R;Wagner, F.F.; Flegel, W.A.
submitted to the EMBL Data Library, July 1995
A:Description: A cDNA, which predicts a protein with PQ-rich repeats, isolated from a ph
A:Reference number: S58222
A:Accession: S58222
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-400 <WAG>
A:Cross-references: UNIPROT:Q15184; EMBL:Z50194; NID:G929659; PIDN:CAA90576.1; PID:G9296

Query Match 16.6%; Score 88; DB 2; Length 400;
Best Local Similarity 34.7%; Pred. No. 0.22; Indels 16; Gaps 4;
Matches 25; Conservative 6; Mismatches 25; Indels 16; Gaps 4;

QY	14	RPKIAHCILFNQPHSPRSNSHSHPNLKLHRRGSHNRPRAYLITILPSKLKLRTHSQS	73
DB	343	QPQQLHPYHPHPH-PHSHPHSHPHP---HPHPHPHQIHPHPH-----PQPHSQP	387
QY	74	H-HNPLSRTSNS	84
DB	388	HGHRLLRSTSNS	399

RESULT 2

T45846
zinc-finger-like protein - Arabidopsis thaliana
N:Alternate names: protein F3A4.10
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45846
R;Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23007
A:Accession: T45846
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-215 <BAR>
A:Cross-references: UNIPROT:Q9SN24; EMBL:AL132978
A:Experimental source: cultivar Columbia; BAC clone F3A4
C:Genetics:
A:Map position: 3
A:Note: F3A4.10

Query Match 15.4%; Score 82; DB 2; Length 215;
Best Local Similarity 29.5%; Pred. No. 0.45; Indels 14; Gaps 4;
Matches 26; Conservative 13; Mismatches 35; Indels 14; Gaps 4;


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Qy 78 LSR-----TSNSTPTNSFLMTSSKPR 98
Db 82 VQRLTGKTSTSTSSYSSTSAK 106

RESULT 7
I50620
Prockr2 - chicken (fragment)
C:Species: Gallus gallus (Chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50620
R:Schutz, B.; Niessing, J.
Gene 148, 227-236, 1994
A:Title: Cloning and structure of a chicken zinc finger cDNA: restricted expression in d
A:Reference number: I50620; MUID:95047430; PMID:7958949
A:Accession: I50620
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1173 <SCH>
A:Cross-references: UNIPROT:Q90783; EMBL:X56805; NID:G577018; PIDN:CAA40140.1; PID:G5770
C:Genetics:
A:Gene: ckr2

Query Match 14.9%; Score 79; DB 2; Length 1173;
Best Local Similarity 30.0%; Pred. No. 5.4;
Matches 27; Conservative 12; Mismatches 21; Indels 30; Gaps 5;

Qy 11 TTNRP-KIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHSHNR-----PRAYILITILP 62
Db 118 TGERPYACSHC-----SKFTTHSSNLLHQRTHSSRSHKCPACPAFV----- 161

Qy 63 SKLKLRTHSOSH-----HNPLSTNSSTP 86
Db 162 SDACLQKHLQSHAASPLLPSPSPQLSP 191

RESULT 8
T43632
serine/threonine protein kinase MIG-15 - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43632
R:Zhu, X.; Acharya, P.; Hedgecock, E.
Submitted to the EMBL Data Library, August 1998
A:Description: MIG-15, a NIK ortholog of the STE20 family of serine/threonine protein ki
A:Reference number: Z22584
A:Accession: T43632
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-728 <ZHU>
A:Cross-references: UNIPROT:Q9XYC4; EMBL:AF0871133; PIDN:AAD14595.1
C:Genetics:
A:Map position: X
A:Note: mig-15
C:Function:
A:Description: probably involved in cell migration and signal transduction

Query Match 14.6%; Score 77.5; DB 2; Length 728;
Best Local Similarity 27.9%; Pred. No. 4.6;
Matches 24; Conservative 13; Mismatches 32; Indels 17; Gaps 3;

Qy 29 PRNSHSHNPPLKLRHRRSHSHNRPRAYILITILP SKLKLRT-----HSQSHH-NPLS 79
Db 52 PRHSPASRPVPVSHHQSPQOSHAPAPHLADLANYEKKRRSRERERERERQAHHAMPIA 111

Qy 80 RTSNSTP-----TNSFLMTSSKP 97
Db 112 RVASVPAPOQSRKMSPELLITHVKP 137

RESULT 9
T43630
serine/threonine protein kinase homolog - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43630
R:Zhu, X.; Acharya, P.; Hedgecock, E.
Submitted to the EMBL Data Library, August 1998
A:Description: MIG-15, a NIK ortholog of the STE20 family of serine/threonine protein ki
A:Reference number: Z22584
A:Accession: T43630
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-792 <ZHU>
A:Cross-references: UNIPROT:Q9UAN7; EMBL:AF0871132; PIDN:AAD14594.1
C:Genetics:
A:Map position: X
A:Note: mig-15

Query Match 14.6%; Score 77.5; DB 2; Length 792;
Best Local Similarity 27.9%; Pred. No. 5;
Matches 24; Conservative 13; Mismatches 32; Indels 17; Gaps 3;

Qy 29 PRNSHSHNPPLKLRHRRSHSHNRPRAYILITILP SKLKLRT-----HSQSHH-NPLS 79
Db 125 PRHSPASRPVPVSHHQSPQOSHAPAPHLADLANYEKKRRSRERERERERQAHHAMPIA 184

Qy 80 RTSNSTP-----TNSFLMTSSKP 97
Db 185 RVASVPAPOQSRKMSPELLITHVKP 210

RESULT 10
T27622
hypothetical protein ZC504.4a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27622
R:Kershaw, J.
Submitted to the EMBL Data Library, July 1995
A:Reference number: Z20394
A:Accession: T27622
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1080 <WIL>
A:Cross-references: UNIPROT:Q23356; EMBL:Z50029; PIDN:CAA90344.1; GSPDB:GN000028; CESP:ZC504
C:Experimental source: clone ZC504
C:Genetics:
A:Gene: CESP:ZC504.4a
A:Map position: X
A:Introns: 15/3; 71/3; 137/3; 211/1; 259/1; 388/2; 428/3; 614/3; 643/3; 680/3; 841/3; 95/3;

Query Match 14.6%; Score 77.5; DB 2; Length 1080;
Best Local Similarity 27.9%; Pred. No. 6.9;
Matches 24; Conservative 13; Mismatches 32; Indels 17; Gaps 3;

Qy 29 PRNSHSHNPPLKLRHRRSHSHNRPRAYILITILP SKLKLRT-----HSQSHH-NPLS 79
Db 413 PRHSPASRPVPVSHHQSPQOSHAPAPHLADLANYEKKRRSRERERERERQAHHAMPIA 472

Qy 80 RTSNSTP-----TNSFLMTSSKP 97
Db 473 RVASVPAPOQSRKMSPELLITHVKP 498

RESULT 11
T17428
PK506 polyketide synthase - Streptomyces sp. (strain MA6548)
C:Species: Streptomyces sp.
A:Variety: strain MA6548
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 12-Jul-2004
C:Accession: T17428
R:Motamedi, H.; Shafiee, A.
Eur. J. Biochem. 256, 528-534, 1998
A:Title: The biosynthetic gene cluster for the macrolactone ring of the immunosuppressan
```

```
Qy 78 LSR-----TSNSTPTNSFLMTSSKPR 98
Db 82 VQRLTGKTSTSTSSYSSTSAK 106

RESULT 7
I50620
Prockr2 - chicken (fragment)
C:Species: Gallus gallus (Chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50620
R:Schutz, B.; Niessing, J.
Gene 148, 227-236, 1994
A:Title: Cloning and structure of a chicken zinc finger cDNA: restricted expression in d
A:Reference number: I50620; MUID:95047430; PMID:7958949
A:Accession: I50620
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1173 <SCH>
A:Cross-references: UNIPROT:Q90783; EMBL:X56805; NID:G577018; PIDN:CAA40140.1; PID:G5770
C:Genetics:
A:Gene: ckr2

Query Match 14.9%; Score 79; DB 2; Length 1173;
Best Local Similarity 30.0%; Pred. No. 5.4;
Matches 27; Conservative 12; Mismatches 21; Indels 30; Gaps 5;

Qy 11 TTNRP-KIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHSHNR-----PRAYILITILP 62
Db 118 TGERPYACSHC-----SKFTTHSSNLLHQRTHSSRSHKCPACPAFV----- 161

Qy 63 SKLKLRTHSOSH-----HNPLSTNSSTP 86
Db 162 SDACLQKHLQSHAASPLLPSPSPQLSP 191

RESULT 8
T43632
serine/threonine protein kinase MIG-15 - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43632
R:Zhu, X.; Acharya, P.; Hedgecock, E.
Submitted to the EMBL Data Library, August 1998
A:Description: MIG-15, a NIK ortholog of the STE20 family of serine/threonine protein ki
A:Reference number: Z22584
A:Accession: T43632
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-728 <ZHU>
A:Cross-references: UNIPROT:Q9XYC4; EMBL:AF0871133; PIDN:AAD14595.1
C:Genetics:
A:Map position: X
A:Note: mig-15
C:Function:
A:Description: probably involved in cell migration and signal transduction

Query Match 14.6%; Score 77.5; DB 2; Length 728;
Best Local Similarity 27.9%; Pred. No. 4.6;
Matches 24; Conservative 13; Mismatches 32; Indels 17; Gaps 3;

Qy 29 PRNSHSHNPPLKLRHRRSHSHNRPRAYILITILP SKLKLRT-----HSQSHH-NPLS 79
Db 52 PRHSPASRPVPVSHHQSPQOSHAPAPHLADLANYEKKRRSRERERERERQAHHAMPIA 111

Qy 80 RTSNSTP-----TNSFLMTSSKP 97
Db 112 RVASVPAPOQSRKMSPELLITHVKP 137

RESULT 9
T43630
serine/threonine protein kinase homolog - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43630
R:Zhu, X.; Acharya, P.; Hedgecock, E.
Submitted to the EMBL Data Library, August 1998
A:Description: MIG-15, a NIK ortholog of the STE20 family of serine/threonine protein ki
A:Reference number: Z22584
A:Accession: T43630
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-792 <ZHU>
A:Cross-references: UNIPROT:Q9UAN7; EMBL:AF0871132; PIDN:AAD14594.1
C:Genetics:
A:Map position: X
A:Note: mig-15

Query Match 14.6%; Score 77.5; DB 2; Length 792;
Best Local Similarity 27.9%; Pred. No. 5;
Matches 24; Conservative 13; Mismatches 32; Indels 17; Gaps 3;

Qy 29 PRNSHSHNPPLKLRHRRSHSHNRPRAYILITILP SKLKLRT-----HSQSHH-NPLS 79
Db 125 PRHSPASRPVPVSHHQSPQOSHAPAPHLADLANYEKKRRSRERERERERQAHHAMPIA 184

Qy 80 RTSNSTP-----TNSFLMTSSKP 97
Db 185 RVASVPAPOQSRKMSPELLITHVKP 210

RESULT 10
T27622
hypothetical protein ZC504.4a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27622
R:Kershaw, J.
Submitted to the EMBL Data Library, July 1995
A:Reference number: Z20394
A:Accession: T27622
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1080 <WIL>
A:Cross-references: UNIPROT:Q23356; EMBL:Z50029; PIDN:CAA90344.1; GSPDB:GN000028; CESP:ZC504
C:Experimental source: clone ZC504
C:Genetics:
A:Gene: CESP:ZC504.4a
A:Map position: X
A:Introns: 15/3; 71/3; 137/3; 211/1; 259/1; 388/2; 428/3; 614/3; 643/3; 680/3; 841/3; 95/3;

Query Match 14.6%; Score 77.5; DB 2; Length 1080;
Best Local Similarity 27.9%; Pred. No. 6.9;
Matches 24; Conservative 13; Mismatches 32; Indels 17; Gaps 3;

Qy 29 PRNSHSHNPPLKLRHRRSHSHNRPRAYILITILP SKLKLRT-----HSQSHH-NPLS 79
Db 413 PRHSPASRPVPVSHHQSPQOSHAPAPHLADLANYEKKRRSRERERERERQAHHAMPIA 472

Qy 80 RTSNSTP-----TNSFLMTSSKP 97
Db 473 RVASVPAPOQSRKMSPELLITHVKP 498

RESULT 11
T17428
PK506 polyketide synthase - Streptomyces sp. (strain MA6548)
C:Species: Streptomyces sp.
A:Variety: strain MA6548
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 12-Jul-2004
C:Accession: T17428
R:Motamedi, H.; Shafiee, A.
Eur. J. Biochem. 256, 528-534, 1998
A:Title: The biosynthetic gene cluster for the macrolactone ring of the immunosuppressan
```


Search completed: October 11, 2005, 07:01:38
Job time : 17.1979 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 58.8262 Seconds
(without alignments)
853.085 Million cell updates/sec

Title: US-10-092-934-6

Perfect score: 531

Sequence: 1 EAYYMLHPTTNRPKIAHC.....SRTSNSTPTNSFLMTSSKPR 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90.5	17.0	305	2 Q9YPF7	Q9ypf7 human herpe
2	88.5	16.7	145	2 Q8N2Q6	Q8n2q6 homo sapien
3	88.5	16.7	1671	2 Q7SE26	Q7se26 neurospora
4	88	16.6	348	2 Q8WV24	Q8wv24 homo sapien
5	88	16.6	400	2 Q15184	Q15184 homo sapien
6	87	16.4	587	2 Q8FRP8	Q8frp8 corynebacte
7	86.5	16.3	1311	2 Q9VXJ5	Q9vxj5 drosophila
8	85.5	16.1	2958	2 Q9VDY5	Q9vdy5 drosophila
9	85	16.0	52	2 Q9NZ17	Q9nzt7 homo sapien
10	85	16.0	356	2 Q8SY01	Q8sy01 drosophila
11	85	16.0	612	2 Q8AXX1	Q8axx1 brachydanio
12	85	16.0	717	2 Q9VW27	Q9vw27 drosophila
13	85	16.0	891	2 Q8IB61	Q8ib61 plasmodium
14	84	15.8	372	2 Q8LC22	Q8lc22 arabidopsis
15	83.5	15.7	720	1 Z408 HUMAN	Q9h9d4 homo sapien
16	83	15.6	502	2 Q7S315	Q7s315 neurospora
17	83	15.6	1379	2 Q7RY49	Q7ry49 neurospora
18	82.5	15.5	226	2 Q8N850	Q8n8e0 homo sapien
19	82	15.4	215	2 Q8SN24	Q8sn24 arabidopsis
20	82	15.4	623	2 P90533	P90533 dictyosteli
21	81.5	15.3	1399	2 Q9W437	Q9w427 drosophila
22	81	15.3	261	2 Q62392	Q62392 mus musculu
23	81	15.3	340	1 LRPI HHV1F	P17588 human herpe
24	80.5	15.2	272	2 Q69079	Q69079 human herpe
25	80.5	15.2	365	1 Y023_CABEL	Q9452 caenorhabdi
26	80.5	15.2	670	1 DOT6_YEAST	P40059 saccharomyc
27	80.5	15.2	1111	2 Q9FH74	Q9fh74 arabidopsis
28	80	15.1	233	2 Q8MP30	Q8mp30 dictyosteli
29	80	15.1	260	2 Q96NM2	Q96nm2 homo sapien
30	79.5	15.0	239	2 Q9LMP5	Q9lmp5 arabidopsis
31	79.5	15.0	329	2 Q8NIY1	Q8niy1 neurospora

ALIGNMENTS

RESULT 1

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Q9YPF7 PRELIMINARY; PRT; 305 AA.
AC Q9YPF7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Latency associated transcript.
OS Human herpesvirus 1 (HHV-1) (Human herpes simplex virus 1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN [1]
RX MEDLINE=88155754; PubMed=2831380;
RA Wagner E.K., Devi-Rao G.B., Feldman L.T., Dobson A.T., Zhang Y.-K.,
RA Flanagan W.M., Stevens J.G.;
RT "Physical characterization of the herpes simplex virus latency-
associated transcript in neurons.";
RL J. Virol. 62:1194-1202(1988).
DR EMBL; M17921; AAA45797.1; -.
SQ SEQUENCE 305 AA; 33087 MW; 994D3762BA4B82F4 CRC64;

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Query Match 17.0%; Score 90.5; DB 2; Length 305;
Best Local Similarity 31.6%; Pred. No. 0.54; Mismatches 7; Indels 23; Gaps 4;
Matches 31; Conservative
QY 9 LPTNRPKIAHCILFNQSPRNSHSPN-----PLKLHRRSHSHNRPRAYILIT 59
Db 39 LPTPTPTPHS---HAPPLPRTPTPHSHAPPLPRTPTPTPHSHAPPLPR-----T 90
QY 60 ILPSKLRTHSOSHNPRLSRTNSSTPTNSFLMTSSKP 97
Db 91 PTP-----THPSHAPPLPRTPTAIHTQTGKRYKSKP 122

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RESULT 2

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Q8N2Q6 PRELIMINARY; PRT; 145 AA.
AC Q8N2Q6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ90047.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A.
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,

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RA Masuko Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074528; BAC11041.1; -.
SQ SEQUENCE 145 AA; 16153 MW; BF44C8E658ECAC2E CRC64;

Query Match 16.7%; Score 88.5; DB 2; Length 145;
Best Local Similarity 30.7%; Pred. No. 0.37;
Matches 23; Conservative 6; Mismatches 13; Indels 33; Gaps 3;

QY 28 SPRSNSSHSHNPL-----KLHRRSHSHNRPRAYILITLPSKILKLRTHSQSHN- 76
Db 65 TPSSHPHQHHPHYTTPSPPLNLRHRRPHSHPR-----LHTTRPHHHL 109
QY 77 -----PLSRTSNS 84
Db 110 PRVTAAPLHRPENS 124

RESULT 3
Q7SE26 PRELIMINARY; PRT; 1671 AA.
AC Q7SE26;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=NCU02768.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR743;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Barrett E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Marcotte E., Gherre S.,
RA Kamal M., Kamysellis M., Mauceli E., Bieleke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Volker R.,
RA Yarden O., Planann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABX01000039; EAA35027.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR007219; Fungal_trans.
DR InterPro; IPR021173; PfkB.
DR Pfam; PF04082; Fungal_trans; 1.
DR PROSITE; PS00583; PFKE_KINASES_1; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 1671 AA; 182498 MW; CRCDSB90957DA706 CRC64;

Query Match 16.7%; Score 88.5; DB 2; Length 1671;
Best Local Similarity 32.0%; Pred. No. 5.7;
Matches 24; Conservative 12; Mismatches 24; Indels 15; Gaps 3;

QY 10 PTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHSHNRPRAYILITLPSKILK 66
Db 1536 PPSSTPATAHI-----PIPTTHAHHPN-----SYQHHPHPRAYITTSIPSRDTLLP 1583
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QY 67 LRTHSQSHHNPLSRT 81
Db 1584 LCTVPTATHNRNRS 1598

RESULT 4
Q8WV24 PRELIMINARY; PRT; 348 AA.
AC Q8WV24;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE PHLDA1 protein (Fragment).
GN Name=PHLDA1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=uterus;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018929; AAH18929.2; -.
DR SMART; SM00233; PH; 1.
FT NON TER 1.
SQ SEQUENCE 348 AA; 38924 MW; 6637BE6D821FB6A4 CRC64;

Query Match 16.6%; Score 88; DB 2; Length 348;
Best Local Similarity 34.7%; Pred. No. 1.1;
Matches 25; Conservative 6; Mismatches 25; Indels 16; Gaps 4;

QY 14 RPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHSHNRPRAYILITLPSKILK 73
Db 291 QPQLHYPYHPHPH-PSHSPHSHPH-HPHPHPHQIHPHP-----PQHSQP 335
QY 74 H-HNPLSRTSNS 84
Db 336 HGHRLLRRTSNS 347

RESULT 5
Q15184 PRELIMINARY; PRT; 400 AA.
AC Q15184;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
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DE PO-rich protein (Apoptosis-associated nuclear protein).
GN Name=PHLDA1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Wagner F.F., Flegel W.A.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kuske M.D.A., Johnson J.P.;
RT "Assignment of the human PHLDA1 (TDAG51) gene to chromosome 12 band
RT q15 by radiation hybrid mapping.";
RL Cytogenet. Cell Genet. 0:0-0(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Gerlinger M., Johnson J.J.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50194; CAA90576.1; -.
DR EMBL; AF239986; AAF64165.1; -.
DR PIR; S58222; S58222.
DR Genew; HGNC:8933; PHLDA1.
DR GO; GO:0005634; C:nucleus; IEA.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH_related.
DR SMART; SM00233; PH; 1.
KW Nuclear protein.
SQ SEQUENCE 400 AA; 4488 MW; 941CC500C57046DD CRC64;

Query Match 16.6%; Score 88; DB 2; Length 400;
Best Local Similarity 34.7%; Pred. No. 1.3;
Matches 25; Conservative 6; Mismatches 25; Indels 16; Gaps 4;

QY 14 RPXIAHCILFNQPHSPRSHSHNPVLKLRHSHSHNPRAVILITLPKLRTHSQS 73
DB 343 QPQQLHPYPHPHPH-PSHSPHSHHPH--HPHPHPHPHPH-----POPHSQP 387
QY 74 H-HNPLSRSTNS 84
DB 388 HGHRLLRSTNS 399

RESULT 6
Q8FRP8 PRELIMINARY; PRT; 587 AA.
AC Q8FRP8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative amino-acid permease.
GN OrderedLocusNames=CE0711;
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314;
RX MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Ikemura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeno K.,
RA Gotohori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens.";
RL Genome Res. 13:1572-1579(2003).
DR EMBL; AP005216; BAC17521.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.

DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/permease.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 587 AA; 62335 MW; 226D58982B764476 CRC64;

Query Match 16.4%; Score 87; DB 2; Length 587;
Best Local Similarity 34.4%; Pred. No. 2.5;
Matches 21; Conservative 10; Mismatches 30; Indels 0; Gaps 0;

QY 29 PRGNSHSHNPVLKLRHSHSHNPRAVILITLPKLRTHSQSHHNPRLSRSTNSPTN 88
DB 509 PRNRAHPHPVALESPRNSHTAAAPPATWTPDPDVTGTEATGHAESARISTRSTG 568
QY 89 S 89
DB 569 T 569

RESULT 7
Q9VXJ5 PRELIMINARY; PRT; 1311 AA.
AC Q9VXJ5; Q9VXJ6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG32577-PA.
GN Name=disco-T; ORFNames=CG32577;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houch J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclbb J.M.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resse M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
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RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
RP [4]
RX SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Smith C.D., Huang Y., Minkler J.S., Millburn G.H., Prochuk S.E.,
RA Hradecky P., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celisner S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN [5]
RG SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE03725; AAF55654.2; -.
DR FlyBase; FBgn0038693; CG5237.
DR InterPro; IPR000345; CytC_heme_BS.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 1.
SQ SEQUENCE 2958 AA; 325706 MW; 86763328F59947F3 CRC64;

Query Match 16.1%; Score 85.5; DB 2; Length 2958;
Best Local Similarity 26.4%; Pred. No. 21;
Matches 23; Conservative 13; Mismatches 32; Indels 19; Gaps 3;

QY 11 TTRNPKIACILFNQPHS--PRNSHSHNPPLKLRHSHNRPR-----AYILITILP 62
Db 1339 SSSRPKPPCPVQSAHTAPFYTHHHHPGHHPYHPHPHHHHHAGSAHVATTATT 1398

QY 63 SKULRTHSQ-----SHNPL 78
Db 1399 SAGLVSTHSQSHQVLRHCVPSPSHSPM 1425

RESULT 9
Q9NZ17 Q9NZ17 PRELIMINARY; PRT; 52 AA.
AC Q9NZ17;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Apoptosis-associated nuclear protein PHLDAL (Fragment).
GN Name=PHLDAL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20354976; PubMed=10894922;
RA Kuske M.D., Johnson J.P.;
RT "Assignment of the human PHLDAL gene to chromosome 12q15 by radiation
RT hybrid mapping.";
RL Cytogenet. Cell Genet. 89:1-1(2000).
[2]
RP SEQUENCE FROM N.A.
RA Kuske M.D., Johnson J.P.;
RT "PHRIP: a novel differentially expressed mRNA in metastatic
RT melanoma.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220656; AAF36387.1; -.
GO; GO:0005634; C:nucleus; IEA.
KW Nuclear protein.
FT NON TER 1
SQ SEQUENCE 52 AA; 5969 MW; 3E616AB55EC13BD9 CRC64;

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Query Match 16.0%; Score 85; DB 2; Length 52;
Best Local Similarity 35.9%; Pred. No. 0.26;
Matches 23; Conservative 5; Mismatches 20; Indels 16; Gaps 4;

QY 23 FNOPH-SPRNSHSHNPPLKLRHSHNRPRAYILITILPSKLKLRTHSQSH-HNPLSR 80
Db 2 YPHPHPHPHSHSHHPH---HHPHPHQIHPHP-----PQPHSQPHGHRLLRS 47

QY 81 TSNS 84
Db 48 TSNS 51

RESULT 10
Q8SY01 Q8SY01 PRELIMINARY; PRT; 356 AA.
AC Q8SY01;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE RE33994p.
GN ORFNames=CG8780;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celisner S.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY075473; AAL68285.1; -.
DR FlyBase; FBgn0036899; CG8780.
SQ SEQUENCE 356 AA; 36699 MW; 4F453F17950BD9EA CRC64;

Query Match 16.0%; Score 85; DB 2; Length 356;
Best Local Similarity 28.0%; Pred. No. 2.2;
Matches 23; Conservative 15; Mismatches 28; Indels 16; Gaps 4;

QY 11 TTRNPKI-----AHCILFNQPHSPRNSHSHNPPLKLRHSHNRPRAYILI 58
Db 209 STSNPAISTATSSVAVSMASHLAASSPHHPHPTHASHPHPL-AHPAHSHHHVGH--V 265

QY 59 TILPSKLKLRTHSQSHNPLS 79
Db 266 GAPPVSTAVTTHHMAHPHPLS 287

RESULT 11
Q8AXX1 Q8AXX1 PRELIMINARY; PRT; 612 AA.
AC Q8AXX1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative gag protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=14963102; DOI=10.1093/molbev/msh072;
RA Goodwin T.J., Poulter R.T.;
RT "A new group of tyrosine recombinase-encoding retrotransposons.";
RL Mol. Biol. Evol. 21:746-759(2004).

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RN  [2]
RP  SEQUENCE FROM N.A.
RL  Goodwin T.J.D., Poulter R.T.M.;
DR  Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
SQ  EMBL: AY152729; AAN71720.1; -
    SEQUENCE 612 AA; 66457 MW; 9A0140DC6C3F1D9D CRC64;

Query Match      16.0%; Score 85; DB 2; Length 612;
Best Local Similarity 34.0%; Pred. No. 4.1;
Matches 33; Conservative 11; Mismatches 31; Indels 22; Gaps 7;

QY  10 PTTNRPKIAHCILFNOPHS-----PRSNSHSHNPCLKHRR--SHSHNRPAYILI 61
Db  213 PLANISTISHA---NOPTTSLTWPPAPHSSTSPSP-PLHTTAISHSHSQPP-----IPNL 264

QY  62 PSKCLKLRTHSQSHNPRTSNTP-TNSFLMTSSKP 97
Db  265 P-----RTSTQLHTTSSSHHNAQPLSNPTLSIPP 296

RESULT 12
Q9VM27 PRELIMINARY; PRT; 717 AA.
AC Q9VM27
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG8780-PA.
GN ORFNames=CG8780;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielieta A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mikhlov G., Milshina N.V., Mobery C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter

```

RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.B., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]

RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]

RP SEQUENCE FROM N.A.
 RX MEDLINE=22426089; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]

RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB003516; AAF49126.2; -
 DR IntAct; Q9VM27; -
 DR FlyBase; FBgn0036899; CG8780.
 SQ SEQUENCE 717 AA; 76715 MW; 887D6033BD9FF679 CRC64;

Query Match 16.0%; Score 85; DB 2; Length 717;
 Best Local Similarity 28.0%; Pred. No. 4.9;
 Matches 23; Conservative 15; Mismatches 28; Indels 16; Gaps 4;

QY 11 TTNRPKI-----AHCILFNQPHSPNSHSHNPCLKHRRSHSHNRPAYILI 58
 Db 209 STSNPAISTATSSVAVSMASHLAASPHHPHTHAHSHPHPL-AHPHAHSHHHVGH--V 265
 QY 59 TILPSKCLKLRT-HSQSHNPLS 79
 Db 266 GAPPVSTAVTTHHMAHPHPLS 287

RESULT 13

Q81B61 PRELIMINARY; PRT; 891 AA.
 AC Q81B61
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein MAJ8P1.45.
 GN Name=MAJ8P1.45;
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

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OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL844507; CAD51147.1; -.
DR InterPro: IPR000884; TSP1.
DR SMART: SM00209; TSP1; 1.
DR PROSITE: PS00092; TSP1; 1.
KW Hypothetical protein.
SQ SEQUENCE 891 AA; 107237 MW; 4765013F17B51B46 CRC64;

Query Match 16.0%; Score 85; DB 2; Length 891;
Best Local Similarity 28.9%; Pred. No. 6.3;
Matches 26; Conservative 8; Mismatches 24; Indels 32; Gaps 4;

Qy 18 AHCLIFNQPHS---PRSNSHHPNPLKLRHRRSHHNRPRAYILITILPSKLRKLTSHSQS 74
Db 107 SHNSHNSHNSHNSHNSHNSHNS---HNSHSHNSHSHS-----SHNSH 150

Qy 75 HNPUSRTSNST-----PTNSFL 91
Db 151 SNHSHSSTQNSLYHDTNQANFLKPTGFFL 180

RESULT 14
Q8LC22 PRELIMINARY; PRT; 372 AA.
AC Q8LC22
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation."
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY086310; AAM64382.1; -.
DR InterPro: IPR011541; NICO_transpt.
DR Pfam: PF03824; NICO; 1.
KW Hypothetical protein.
SQ SEQUENCE 372 AA; 39686 MW; 9FDB12077B5B3FFA CRC64;

Query Match 15.8%; Score 84; DB 2; Length 372;
Best Local Similarity 33.3%; Pred. No. 3;
Matches 30; Conservative 13; Mismatches 25; Indels 22; Gaps 6;

Qy 14 RPKIAHCILFNQPHSPRSNSHHPNPLKLRHRRSHHNRPRAYILITILPSKLRKLTSHSQS 73
Db 6 QPPSSHSI-----AP-SKTQSRSPLLH-RLHSPN-----LTFPPSSRLLESRRIS 50

Qy 74 -----HNNPLSRTS-NSTPTNSFLMTSSK 96
Db 51 SISCFFRRHNPDLPTSPGINSQSNFLIASQ 80

RESULT 15
Z408_HUMAN

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ID AC
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Zinc finger protein 408 (PR-domain zinc finger protein 17).
GN Name=ZNF408; Synonyms=PFM14, PRDM17;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Du Y., Huang S.;
RT "A family of novel PR-domain (PRDM) genes as candidate tumor
RT suppressors."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ora T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahata T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuna M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togishi S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Inose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Komatsu T.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45(2004).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung and Uterus;
RL PubMed=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fanev J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

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```
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May function as a transcription factor.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: Contains 10 C2H2-type zinc fingers.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF346626; AAK29075.1; -.
DR EMBL; AK022889; BAB14295.1; -.
DR EMBL; BC013355; AAH13355.1; -.
DR EMBL; BC015708; AAH15708.1; -.
DR HSSP; P25490; IUBD.
DR IntAct; Q9H9D4; -.
DR Genew; HGNC:20041; ZNF408.
DR H-InvDB; HIX0009606; -.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00036; zf-C2H2; 10.
DR SMART; SM00355; Znf_C2H2; 10.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 10.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 10.
KW DNA-binding; Metal-binding; Nuclear protein; Repeat;
KW Transcription regulation; Zinc-finger.
FT ZN_FING 353 375 C2H2-type 1.
FT ZN_FING 381 403 C2H2-type 2.
FT ZN_FING 409 431 C2H2-type 3.
FT ZN_FING 437 459 C2H2-type 4.
FT ZN_FING 468 490 C2H2-type 5.
FT ZN_FING 496 518 C2H2-type 6.
FT ZN_FING 524 546 C2H2-type 7.
FT ZN_FING 551 573 C2H2-type 8.
FT ZN_FING 579 601 C2H2-type 9.
FT ZN_FING 607 629 C2H2-type 10.
SQ SEQUENCE 720 AA; 78438 MW; 0D3CDA7572D17721 CRC64;

Query Match 15.7%; Score 83.5; DB 1; Length 720;
Best Local Similarity 33.3%; Pred. No. 7;
Matches 31; Conservative 5; Mismatches 26; Indels 31; Gaps 5;

QY 7 LHLPTTNRP-KIAHCI-LFNQPHSPRSNSHSH-----PNEPLKHERSHS 48
Db 515 LRLTGERPYRCHCADAFQLPFLRRHLISHTGEAHLCPVCGKALRDPHTLRAHERLHS 574

QY 49 HNRP-----RAYILITILPSKLRTHSQSH 74
Db 575 GERPPPCPGGRAYTLAT-----KLRRHLKSH 601

Search completed: October 11, 2005, 07:18:49
Job time : 61.8262 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 72.5829 Seconds
(without alignments)
522.196 Million cell updates/sec

Title: US-10-092-934-6

Perfect score: 531

Sequence: 1 EAYTMLHLPTTRPKIAHC.....SRTSNSTPTNSFLMTSSKPR 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	531	100.0	98	2	AAR63235
2	531	100.0	98	2	AAR95914
3	531	100.0	98	5	AAE29147
4	531	100.0	98	6	ABR63245
5	531	100.0	98	6	ABU02977
6	531	100.0	98	6	ABP59927
7	531	100.0	98	6	AAE33194
8	531	100.0	98	6	ABJ19450
9	531	100.0	98	7	ADB37524
10	531	100.0	98	7	ADL96025
11	500	94.2	147	4	AAE63838
12	117	22.0	23	6	ABP59910
13	117	22.0	23	7	ADL96056
14	89.5	16.9	185	5	ABJ03679
15	88.5	16.7	145	4	AM933210
16	88.5	16.7	145	8	ADL30575
17	88	16.6	151	4	ABG29454
18	88	16.6	259	8	ADO20034
19	88	16.6	259	8	ADP22472
20	88	16.6	259	8	ADP55210
21	88	16.6	259	8	ADP24864
22	88	16.6	400	7	ADD18728
23	88	16.6	400	7	ADF76875
24	88	16.6	400	8	ADQ18293
25	88	16.6	445	5	ADJ33773

26	86.5	16.3	682	4	ABG03784	Novel hum
27	86	16.2	15	6	ABP59906	Human neu
28	86	16.2	15	7	ADL96052	Human neu
29	85.5	16.1	2958	4	ABB71368	Drosophila
30	85	16.0	15	6	ABP59907	Human neu
31	85	16.0	15	7	ADL96053	Human neu
32	85	16.0	525	5	ABA47787	Protein e
33	85	16.0	525	7	ADM86624	Aspergill
34	85	16.0	793	4	ABB71688	Drosophila
35	84	15.8	15	6	ABP59905	Human neu
36	84	15.8	15	7	ADL96051	Human neu
37	84	15.8	197	3	AAG58875	Arabidops
38	84	15.8	207	3	AAG58874	Arabidops
39	84	15.8	372	3	AAG58870	Arabidops
40	83.5	15.7	273	4	AAU16468	Human nov
41	83.5	15.7	273	6	ABU55537	Human nov
42	83.5	15.7	316	4	AAU16083	Human nov
43	83.5	15.7	316	6	ABU55152	Human nov
44	83.5	15.7	450	5	ABB97178	Novel hum
45	83.5	15.7	720	4	AAB94329	Human pro

ALIGNMENTS

RESULT 1
AAR63235
ID AAR63235 standard; protein; 98 AA.
XX AAR63235;
AC AAR63235;
XX 25-MAR-2003 (revised)
DT 06-JUL-1995 (first entry)
XX
XX CNS neural thread protein HB4.
XX
XX Central nervous system; neural thread protein HB4; Alzheimer's;
KW neuroectodermal tumours; malignant astrocytomas; glioblastomas.
XX
XX Homo sapiens.
XX
XX WO9423756-A1.
XX
XX PD
XX 27-OCT-1994.
XX
XX 20-APR-1994; 94WO-US004321.
XX
XX 20-APR-1993; 93US-00050559.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX
XX De La Monte SM, Wands JR;
XX
XX WPI; 1994-341497/42.
XX
XX N-PSDB; AAQ77871.
XX
XX Detection of neural thread proteins - to detect sporadic and familial
PT Alzheimer's disease, neuroectodermal tumours, malignant astrocytomas and
PT glioblastomas (Eng).
XX
XX Example 4; Fig 11a; 158pp; English.
XX
XX AAQ77870 encodes AAR63235 the HB4 CNS neural thread protein (NTP). These
CC sequences were used in the development of an antibody dependent method,
CC for the detection of NTPs. This new method could be used to diagnose
CC Alzheimer's disease (differentiating between sporadic and familial),
CC neuroectodermal tumours, malignant astrocytomas and glioblastomas.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 98 AA;
SQ
Query Match 100.0%; Score 531; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.5e-53;

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Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EAYYTMLHLPPTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHSHNRPRAYILITI 60
Db 1 EAYYTMLHLPPTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHSHNRPRAYILITI 60
Qy 61 LPSKCLKRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
Db 61 LPSKCLKRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98

RESULT 2
AAR95914
ID AAR95914 standard; protein; 98 AA.
XX
AC AAR95914;
XX
DT 14-NOV-1996 (first entry)
XX
DE HB4 human neural thread protein partial sequence.
XX
KW Neural thread protein; NTP; hyperplasia; hypertrophy; arteriosclerosis;
KW haemorrhoid; gene therapy; tumour; vascular disease; atherosclerosis;
KW inflammatory disease; nutritional deficiency disease; genetic disease;
KW autoimmune disease; metabolic disease; traumatic disease; intoxication;
KW amyloid disease; congenital malformation; enzyme deficiency disease;
KW poisoning; environmental disease; storage disease; radiation disease;
KW degenerative disease; endocrine disease; protein therapy;
XX
OS Unidentified.
XX
PN WO200274323-A2.
XX
PD 26-SEP-2002.
XX
PF 08-MAR-2002; 2002WO-1B001959.
XX
PR 08-MAR-2001; 2001US-0273957P.
XX
PA (AVER/) AVERBACK P.
XX
PI Averbach P;
XX
XX WPI; 2002-759864/82.
XX
PT Treating a condition in a patient requiring removal or destruction of
PT cells, such as a benign or malignant tumor of a tissue or an inflammatory
PT disease, comprises administering a neural thread protein (NTP) or a NTP
PT gene to a mammal.
XX
PS Claim 23; Fig 6; 70pp; English.
XX
CC The invention relates to a method for treating a condition in a patient
CC requiring removal or destruction of cells. The method involves
CC administering to a mammal a neural thread protein (NTP), or administering
CC to a tumour or other target cell a NTP gene, where the expression of the
CC NTP gene is induced resulting in expression of the NTP protein. The
CC method and NTP are useful for treating a condition in a patient requiring
CC removal or destruction of cells, such as a benign or malignant tumour of
CC a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue,
CC preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,
CC bacterially, or parasitically altered tissue, or a malformation of a
CC tissue. Other conditions include a cosmetic modification to a tissue,
CC such as removal of unwanted facial hair, warts or unwanted fatty tissue,
CC a vascular disease, particularly atherosclerosis or arteriosclerosis,
CC haemorrhoids, or varicose veins, an inflammatory disease, autoimmune
CC disease, metabolic disease, hereditary/genetic disease, traumatic disease
CC or physical injury, nutritional deficiency disease, infectious disease,
CC congenital malformation, amyloid disease, fibrosis disease, storage
CC disease, enzyme deficiency disease, poisoning, intoxication, degenerative
CC disease, radiation disease, environmental disease, endocrine disease or
CC mechanical disease. The invention is useful in protein therapy and gene
CC therapy. The present sequence is NTP protein
XX
SQ Sequence 98 AA;
Query Match 100.0%; Score 531; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.5e-53;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EAYYTMLHLPPTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHSHNRPRAYILITI 60
Db 1 EAYYTMLHLPPTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHSHNRPRAYILITI 60
Qy 61 LPSKCLKRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
Db 61 LPSKCLKRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98

Detection of neural thread protein in diagnosis of Alzheimer's disease -
also NTP DNA and protein sequences used in gene and anti:sense therapy.
Example 4b; Fig 11A; 238pp; English.
A method for detecting the presence of neural thread protein (NTP) having
a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject
comprises (a) contacting a sample from a human subject that is suspected
of containing the NTP with at least one molecule capable of binding to
the protein; and (b) detecting any of the molecule bound to the protein.
The binding molecule is selected from an antibody free of natural
impurities, a monoclonal antibody or a binding fragment of either of
these. The method may be used for diagnosing the presence of Alzheimer's
disease, neuroectodermal tumours and a malignant astrocytoma in a human.
A number of clones of neural thread protein were isolated from healthy 17
-18 week old fetal human brain (HB) 2 year old temporal lobe neocortex
and end stage Alzheimer's disease (AD) cerebral cortex. See AAR27753-75
Sequence 98 AA;
Query Match 100.0%; Score 531; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.5e-53;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EAYYTMLHLPPTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHSHNRPRAYILITI 60
Db 1 EAYYTMLHLPPTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHSHNRPRAYILITI 60
Qy 61 LPSKCLKRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
Db 61 LPSKCLKRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
```



```
Db 1 EAYTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRSHSHNRPRAYILIITI 60
QY 61 LPSKILRTHSQSHHNPRLSRTSNSTPTNSFLMTSSKPR 98
Db 61 LPSKILRTHSQSHHNPRLSRTSNSTPTNSFLMTSSKPR 98

RESULT 4
ID ABR63245 standard; protein; 98 AA.
AC ABR63245;
XX
DT 28-AUG-2003 (first entry)
DE 98 amino acid neural thread protein.
XX
KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour.
XX
OS Unidentified.
XX
PN WO2003008443-A2.
XX
PD 30-JAN-2003.
XX
PF 19-JUL-2002; 2002WO-CA001105.
XX
PR 19-JUL-2001; 2001US-0306150P.
PR 19-JUL-2001; 2001US-0306161P.
PR 16-NOV-2001; 2001US-0331477P.
XX
PA (NYMO-) NYMOX CORP.
XX
PI Averbach PA;
XX
WPI; 2003-247999/24.
XX
PT Novel neural thread protein peptide, referred as cell death peptide,
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
XX
PS Disclosure; Fig 6; 77pp; English.
XX
CC The present invention relates to a neural thread protein (NTP) peptide
CC referred to as cell death peptide. Thought to be cytostatic.
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC treating a condition in a patient requiring removal or destruction of
CC cells, for treating a condition such as benign or malignant tumor,
CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for
CC a pancreatic thread protein. The peptide is conjugated, linked or bound
CC to a molecule chosen from antibody or its fragment, antibody-like binding
CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side
CC effects of surgery. The present sequence is an NTP amino acid sequence
XX
SQ Sequence 98 AA;
Query Match 100.0%; Score 531; DB 6; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.5e-53;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EAYTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRSHSHNRPRAYILIITI 60
Db 1 EAYTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRSHSHNRPRAYILIITI 60
QY 61 LPSKILRTHSQSHHNPRLSRTSNSTPTNSFLMTSSKPR 98
Db 61 LPSKILRTHSQSHHNPRLSRTSNSTPTNSFLMTSSKPR 98
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RESULT 5
ABU02977
ID ABU02977 standard; protein; 98 AA.
XX
AC ABU02977;
XX
DT 20-JAN-2003 (first entry)
DE Human neural thread protein AD7C-NTP, protein fragment #5.
XX
KW Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;
KW transplantation; grafting; chemotherapy; immunotherapy; vaccination;
KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;
KW radiation; tumour; hyperplasia; hypertrophy; overgrowth of tissue;
KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;
KW cosmetic modification; vascular disease; atherosclerosis;
KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;
KW autoimmune disease; metabolic disease; traumatic disease;
KW physical injury; nutritional deficiency disease; infectious disease;
KW amyloid disease; fibrosis disease; storage disease;
KW congenital malformation; enzyme deficiency disease; poisoning;
KW intoxication; environmental disease; radiation disease;
KW endocrine disease; degenerative disease; mechanical disease.
XX
OS Homo sapiens.
XX
PN WO200297030-A2.
XX
PD 05-DEC-2002.
XX
PF 24-MAY-2002; 2002WO-CA000759.
XX
PR 25-MAY-2001; 2001US-0293156P.
XX
PA (NYMO-) NYMOX CORP.
XX
PI Averbach PA;
XX
WPI; 2003-041406/03.
XX
PT Novel peptides similar in amino acid sequence to neural thread proteins
PT (NTP), useful for treating unwanted cellular proliferations such as
PT malignant tumors and prostatic hyperplasia.
XX
PS Disclosure; Fig 6; 78pp; English.
XX
CC The invention describes an NTP-peptide (I) comprising at least one amino
CC acid sequence corresponding to part of the amino acid sequence of a
CC neural thread protein, AD7C-NTP. The invention provides a method of
CC treating a condition requiring removal or destruction of cells of a
CC mammal comprising administering to a mammal, a therapeutic amount of (I).
CC The treatment is administered to the mammal before, during or after
CC surgical excision, transplantation, grafting, chemotherapy,
CC immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,
CC laser therapy, phototherapy, gene therapy and/or radiation. The method is
CC useful for treatment of benign or malignant tumour: hyperplasia,
CC hypertrophy or overgrowth of tissue; virally, bacterially or
CC parasitically altered tissue; malformation of tissue selected from lung,
CC sinus, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,
CC gland, blood, brain and its coverings, spinal cord, muscle, connective
CC tissue, adrenal, parathyroid thyroid, uterus, testis, pituitary,
CC reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,
CC tonsils, mouth and lymph nodes and lymphoid system; tonsillary
CC hypertrophy; prostatic hyperplasia; cosmetic modification to a tissue;
CC vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;
CC varicose veins; inflammatory disease; autoimmune disease; metabolic
CC disease; hereditary/genetic disease; traumatic disease; physical injury;
CC nutritional deficiency disease; infectious disease; amyloid disease;
CC fibrosis disease; storage disease; congenital malformation; enzyme
CC deficiency disease; poisoning; intoxication; environmental disease;
CC radiation disease; endocrine disease; degenerative disease and mechanical
```

CC disease. This is the amino acid sequence of a human neural thread protein
 CC AD7C-NTP protein fragment
 XX
 SQ Sequence 98 AA;

Query Match 100.0%; Score 531; DB 6; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.5e-53;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAYYTMLHPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHSHSHNRPRAYILITI 60
 |||||
 DB 1 EAYYTMLHPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHSHSHNRPRAYILITI 60
 |||||
 QY 61 LPSKLRTHSQSHHNPPLSRTNSTPTNSFLMTSSKPR 98
 |||||
 DB 61 LPSKLRTHSQSHHNPPLSRTNSTPTNSFLMTSSKPR 98
 |||||

RESULT 6
 ABP59927
 ID ABP59927 standard; protein; 98 AA.
 XX
 AC ABP59927;
 XX
 DT 08-SEP-2003 (first entry)
 XX
 DE Human 98 amino acid neural thread protein.
 XX
 DE Human; tumour; cancer; neural thread protein; NTP; cell removal;
 KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;
 KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX WO2003044053-A2.
 PN
 XX 30-MAY-2003.
 PD
 XX 18-NOV-2002; 2002WO-CA001757.
 PF
 XX 16-NOV-2001; 2001US-0331477P.
 PR
 XX (NYMO-) NYMOX CORP.
 PA
 XX Averbach P, Gemmell J;
 PI
 XX WPI; 2003-457592/43.
 DR
 XX New neural thread protein (NTP), useful for preparing a composition for
 PT treating or preventing a condition in a mammal requiring removal or
 PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or
 PT inflammatory disease.
 XX
 XX Disclosure; Fig 4; 98pp; English.

XX The present invention relates to peptides derived from the human neural
 CC thread protein (NTP). The peptides are useful for preparing a composition
 CC for treating or preventing a condition in a mammal requiring removal or
 CC destruction of cells, comprising tonsillary hypertrophy, prostatic
 CC hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a
 CC breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,
 CC varicose veins, atherosclerosis, inflammatory, metabolic, infectious,
 CC fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,
 CC occlusion or blockage of an artery or of a stent placed or implanted in
 CC an artery. The present sequence is an NTP protein used to produce
 CC peptides of the invention
 XX
 SQ Sequence 98 AA;

Query Match 100.0%; Score 531; DB 6; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.5e-53;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAYYTMLHPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHSHSHNRPRAYILITI 60
 |||||
 DB 1 EAYYTMLHPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHSHSHNRPRAYILITI 60
 |||||
 QY 61 LPSKLRTHSQSHHNPPLSRTNSTPTNSFLMTSSKPR 98
 |||||
 DB 61 LPSKLRTHSQSHHNPPLSRTNSTPTNSFLMTSSKPR 98
 |||||

RESULT 7
 AAE33194
 ID AAE33194 standard; protein; 98 AA.
 XX
 AC AAE33194;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Neural thread protein (NTP) #5.
 XX
 DE Cell death; tissue necrosis; neural thread protein; NTP; amyloidosis;
 KW stroke; brain tumour; Pick's disease; Parkinson's disease; glaucoma;
 KW Alzheimer's disease; gene therapy.
 KW
 XX Unidentified.
 OS
 XX WO200289841-A2.
 PN
 XX 14-NOV-2002.
 PD
 XX 06-MAY-2002; 2002WO-CA000681.
 PF
 XX 04-MAY-2001; 2001US-0288463P.
 PR
 XX (NYMO-) NYMOX CORP.
 PA
 XX Averbach PA;
 PI
 XX WPI; 2003-120506/11.
 DR
 XX Preventing, controlling, modulating, ameliorating and/or treating cell
 PT death or tissue necrosis using antibodies to neural thread proteins,
 PT useful in disorders such as stroke, brain tumor, glaucoma and Alzheimer's
 PT disease.
 XX
 XX Disclosure; Fig 9; 60pp; English.

XX The invention relates to a method of preventing, and/or inhibiting cell
 CC death and/or tissue necrosis in live tissue containing neural thread
 CC proteins (NTP). The method involves contacting the live tissue with at
 CC least one antibody, fragment or derivative that recognises NTP, where the
 CC antibody, fragment or derivative is present to prevent, control,
 CC ameliorate and/or inhibit cell death and/or tissue necrosis caused by the
 CC presence of NTP. Methods and compositions of the invention are useful for
 CC preventing, modulating, controlling and/or treating disorders associated
 CC with cell death and/or tissue necrosis such as stroke, brain tumour,
 CC Pick's disease, Parkinson's disease, amyloidosis, glaucoma and
 CC Alzheimer's disease. The invention is useful in gene therapy. The present
 CC sequence is NTP protein

SQ Sequence 98 AA;

Query Match 100.0%; Score 531; DB 6; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.5e-53;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAYYTMLHPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHSHSHNRPRAYILITI 60
 |||||
 DB 1 EAYYTMLHPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHSHSHNRPRAYILITI 60
 |||||
 QY 61 LPSKLRTHSQSHHNPPLSRTNSTPTNSFLMTSSKPR 98
 |||||
 DB 61 LPSKLRTHSQSHHNPPLSRTNSTPTNSFLMTSSKPR 98
 |||||

XX AC ADL96025;
XX DT 20-MAY-2004 (first entry)
XX DE Human neural thread protein, NTP98.
XX KW Human; neural thread protein; NTP122; NTP112; NTP106; NTP98; NTP75;
XX KW NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;
XX KW eczema; haemorrhoid; atherosclerosis; inflammatory disease;
XX KW autoimmune disease; metabolic disease; hereditary disease;
XX KW genetic disease; traumatic disease; physical injury;
XX KW nutritional deficiency disease; infectious disease; amyloid disease;
XX KW Alzheimer's disease; storage disease; congenital malformation;
XX KW enzyme deficiency disease; poisoning; intoxication;
XX KW environmental disease; radiation disease; endocrine disease;
XX KW degenerative disease; mechanical disease.
XX OS Homo sapiens.
XX PN US200316569-A1.
XX PD 04-SEP-2003.
XX PF 15-NOV-2002; 2002US-00294891.
XX PR 16-NOV-2001; 2001US-0331477P.
XX PA (AVER/) AVERBACK P.
XX PA (GEMM/) GEMMELL J.
XX PI Averbach P, Gemmell J;
XX DR WPI; 2003-898099/82.
XX PT New neural thread protein or its variants, useful for treating tumors and
XX PT other conditions requiring the removal or destruction of cells (e.g.
XX PT prostatic hyperplasia, psoriasis, eczema, hemorrhoids or
XX PT atherosclerosis).
XX PS Disclosure; SEQ ID NO 4; 32pp; English.
XX CC The invention relates to a peptide, or its homologue, derivative,
XX CC fragment, variant or mimetic, comprising at least one neural thread
XX CC protein (NTP) peptide appearing as ADL96029-ADL96069, derived from
XX CC NTP122, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid
XX CC encoding an amino acid sequence corresponding to the above peptide, a
XX CC composition comprising one or more peptides or nucleic acids cited above
XX CC and a carrier, a method of treating a condition in a mammal requiring
XX CC removal or destruction of cells (comprising administering to the mammal
XX CC an amount of the peptide cited above) and a method of preventing or
XX CC inhibiting the stenosis, occlusion or blockage of a stent, comprising
XX CC coating the stent with an amount of the above peptide. The peptide
XX CC further comprises an amino acid in a reverse-D order based on the above
XX CC amino acid sequences. The composition and methods are useful in treating
XX CC tumours and other conditions requiring the removal or destruction of
XX CC cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or
XX CC atherosclerosis). These may also be used in treating inflammatory
XX CC diseases, autoimmune diseases, metabolic diseases, hereditary/genetic
XX CC diseases, traumatic diseases or physical injuries, nutritional deficiency
XX CC diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,
XX CC storage diseases, congenital malformation, enzyme deficiency diseases,
XX CC poisoning, intoxication, environmental diseases, radiation diseases,
XX CC endocrine diseases, degenerative diseases or mechanical diseases. The
XX CC invention sequence is a human NTP protein from which the peptides of the
XX CC present are derived.
XX SQ Sequence 98 AA;
Query Match 100.0%; Score 531; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.5e-53;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAYYTMHLPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHRRSHSHNRPRAYILITI 60
Db |||||
QY 1 EAYYTMHLPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHRRSHSHNRPRAYILITI 60
Db |||||
QY 61 LPSKLRTHSQSHHNPRLSRTSNSTPTNSFLMTSSKPR 98
Db |||||
QY 61 LPSKLRTHSQSHHNPRLSRTSNSTPTNSFLMTSSKPR 98
Db |||||
RESULT 11
AAB63838
ID AAB63838 standard; protein; 147 AA.
XX AAB63838;
XX AC AAB63838;
XX DT 26-MAR-2001 (first entry)
XX DE Human prostate cancer associated antigen protein sequence SEQ ID NO:1200.
XX KW Human; breast cancer; gastric cancer; prostate cancer; diagnosis;
XX KW cancer associated antigen; cytostatic; cancer vaccine.
XX OS Homo sapiens.
XX PN WO200073801-A2.
XX PD 07-DEC-2000.
XX PF 26-MAY-2000; 2000WO-US014749.
XX PR 28-MAY-1999; 99US-0136526P.
XX PR 10-SEP-1999; 99US-0153454P.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Obata Y;
XX PT WPI; 2001-025274/03.
XX CC Nucleic acids encoding breast, gastric and prostate cancer associated
XX CC antigen precursors, useful for diagnosing and treating a condition
XX CC characterized by expression of an abnormal amount of a protein, e.g.
XX CC cancer.
XX PS Example 1; Page 740-741; 799pp; English.
XX CC AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
XX CC represent nucleotide sequences encoding human breast, gastric and
XX CC prostate cancer associated antigen precursors (CAAP) respectively.
XX CC AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
XX CC represent human breast, gastric and prostate CAAP protein sequence
XX CC respectively. CAAPs have cytostatic activity and can be used in the
XX CC production of cancer vaccines. The human CAAP proteins, peptides, nucleic
XX CC acids or anti-CAAP antibodies are useful for diagnosing and treating a
XX CC condition characterised by expression of an abnormal amount of a protein,
XX CC e.g. cancer
XX SQ Sequence 147 AA;
Query Match 94.2%; Score 500; DB 4; Length 147;
Best Local Similarity 96.8%; Pred. No. 9.9e-50;
Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 YTMHLPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHRRSHSHNRPRAYILITILPS 63
Db |||||
QY 53 YNKLHLPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHRRSHSHNRPRAYILITILPS 112
Db |||||
QY 64 KLKLRTHSQSHHNPRLSRTSNSTPTNSFLMTSSKPR 98
Db |||||
QY 113 KLKLRTHSQSHHNPRLSRTSNSTPTNSFLMTSSKPR 147
Db |||||
RESULT 12

ABP59910
 ID ABP59910 standard; peptide; 23 AA.
 AC ABP59910;
 XX
 XX 28-AUG-2003 (first entry)
 DT
 XX Human neural thread protein NTP(98) peptide #6.
 DE
 XX Human; tumour; cancer; neural thread protein; NTP; cell removal;
 KW cell destruction; antipsoptic; antimicrobial; immunosuppressive;
 KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;
 KW gene therapy.
 KW
 XX
 XX Homo sapiens.
 OS
 XX WO2003044053-A2.
 PN
 XX 30-MAY-2003.
 PD
 XX 18-NOV-2002; 2002WO-CA001757.
 PF
 XX 16-NOV-2001; 2001US-0331477P.
 PR
 XX (NYMO-) NYMOX CORP.
 PA
 XX Averbach P, Gemmell J;
 PI
 XX WPI; 2003-457592/43.
 DR
 XX New neural thread protein (NTP), useful for preparing a composition for
 XX treating or preventing a condition in a mammal requiring removal or
 PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or
 PT inflammatory disease.
 PT
 XX Claim 1; Page 37; 98pp; English.
 PS
 XX The present invention relates to peptides derived from the human neural
 CC thread protein (NTP). The peptides are useful for preparing a composition
 CC for treating or preventing a condition in a mammal requiring removal or
 CC destruction of cells, comprising tonsillary hypertrophy, prostatic
 CC hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a
 CC breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,
 CC varicose veins, atherosclerosis, inflammatory, metabolic, infectious,
 CC fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,
 CC occlusion or blockage of an artery or of a stent placed or implanted in
 CC an artery. The present sequence is a peptide of the invention
 CC
 XX Sequence 23 AA;
 QY Query Match 22.0%; Score 117; DB 6; Length 23;
 DB Best Local Similarity 100.0%; Pred. No. 2.3e-06;
 XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 76 NPLSRTSNSTPTNSFLMTSSKPR 98
 DB 1 NPLSRTSNSTPTNSFLMTSSKPR 23
 RESULT 13
 ADL96056
 ID ADL96056 standard; peptide; 23 AA.
 XX
 XX ADL96056;
 AC
 XX 20-MAY-2004 (first entry)
 DT
 XX Human neural thread protein, NTP98, peptide #6.
 DE
 XX Human; neural thread protein; NTP122; NTP106; NTP98; NTP75;
 KW NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;
 KW eczema; haemorrhoid; atherosclerosis; inflammatory disease;
 KW autoimmune disease; metabolic disease; hereditary disease;

genetic disease; traumatic disease; physical injury;
 nutritional deficiency disease; infectious disease; amyloid disease;
 Alzheimer's disease; storage disease; congenital malformation;
 enzyme deficiency disease; poisoning; intoxication;
 environmental disease; radiation disease; endocrine disease;
 degenerative disease; mechanical disease.
 KW
 XX Homo sapiens.
 OS
 XX US200316569-A1.
 PN
 XX 04-SEP-2003.
 PD
 XX 15-NOV-2002; 2002US-00294891.
 PF
 XX 16-NOV-2001; 2001US-0331477P.
 PR
 XX (AVER/) AVERBACK P.
 PA (GEMM/) GEMMELL J.
 PI Averbach P, Gemmell J;
 XX WPI; 2003-898099/82.
 DR
 XX New neural thread protein or its variants, useful for treating tumors and
 PT other conditions requiring the removal or destruction of cells (e.g.
 PT prostatic hyperplasia, psoriasis, eczema, hemorrhoids or
 PT atherosclerosis).
 PT
 XX Claim 1; SEQ ID NO 35; 32pp; English.
 PS
 XX The invention relates to a peptide, or its homologue, derivative,
 CC fragment, variant or mimetic, comprising at least one neural thread
 CC protein (NTP) peptide appearing as ADL96029-ADL96069, derived from
 CC NTP122, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid
 CC encoding an amino acid sequence corresponding to the above peptide, a
 CC composition comprising one or more peptides or nucleic acids cited above
 CC and a carrier, a method of treating a condition in a mammal requiring
 CC removal or destruction of cells (comprising administering to the mammal
 CC an amount of the peptide cited above) and a method of preventing or
 CC inhibiting the stenosis, occlusion or blockage of a stent, comprising
 CC coating the stent with an amount of the above peptide. The peptide
 CC further comprises an amino acid in a reverse-D order based on the above
 CC amino acid sequences. The composition and methods are useful in treating
 CC tumours and other conditions requiring the removal or destruction of
 CC cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or
 CC atherosclerosis). These may also be used in treating inflammatory
 CC diseases, autoimmune diseases, metabolic diseases, hereditary/genetic
 CC diseases, traumatic diseases or physical injuries, nutritional deficiency
 CC storage diseases, congenital malformation, enzyme deficiency diseases,
 CC poisoning, intoxication, environmental diseases, radiation diseases,
 CC endocrine diseases, degenerative diseases or mechanical diseases. The
 CC present sequence is a NTP peptide of the invention.
 XX
 XX Sequence 23 AA;
 QY Query Match 22.0%; Score 117; DB 7; Length 23;
 DB Best Local Similarity 100.0%; Pred. No. 2.3e-06;
 XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 76 NPLSRTSNSTPTNSFLMTSSKPR 98
 DB 1 NPLSRTSNSTPTNSFLMTSSKPR 23
 RESULT 14
 ABJ03679
 ID ABJ03679 standard; protein; 185 AA.
 XX
 XX ABJ03679;
 AC
 XX 25-SEP-2002 (first entry)
 DT

```
XX DE Human ovary specific protein SEQ ID NO: 121.
XX KW Human; ovary; ovarian cancer; ovarian disease; gene therapy; cytostatic.
XX OS Homo sapiens.
XX PN WO200240720-A2.
XX PD 23-MAY-2002.
XX PF 20-NOV-2001; 2001WO-US045010.
XX PR 20-NOV-2000; 2000US-0249997P.
XX PA (DIAD-) DIADEXUS INC.
XX PI Salceda S, Macina RA, Recipon H, Cafferkey R, Sun Y, Liu C;
XX DR WPI; 2002-547588/58.
XX PT New ovary polypeptides useful for detecting, diagnosing, monitoring,
XX PT treating, staging and imaging cancers in humans having cancer and non-
XX PT cancerous ovary disease.
XX PS Claim 11; Page 233-234; 296pp; English.
XX CC The present invention provides human proteins and coding sequences
XX CC specifically found in ovary cells. These can be used in the diagnosis and
XX CC treatment of ovarian diseases, including cancer. The present sequence is
XX CC a protein of the invention
XX SQ Sequence 185 AA;

Query Match 16.9%; Score 89.5; DB 5; Length 185;
Best Local Similarity 33.0%; Pred. No. 0.046;
Matches 30; Conservative 15; Mismatches 33; Indels 13; Gaps 6;

QY 4 YTMHLPTTRPKIAICILFNQPHSPR--SNSSHNPPLKLRP-SHSHNRPRAYILITI 60
Db 100 HTSPHPTVNH--LSHPLNQPHHRLDSSPTHP-PLHIHKOINHTSAPHNTHTRSTL 156

QY 61 LPSEKLRTHSQSHHNPPLSRSTNSPTNSPL 91
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ID AAM93210 standard; protein; 145 AA.
XX AC AAM93210;
XX DT 06-NOV-2001 (first entry)
XX DE Human polypeptide, SEQ ID NO: 2608.
XX KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX OS Homo sapiens.
XX PN EP1130094-A2.
XX PD 05-SEP-2001.
XX PF 07-JUL-2000; 2000EP-00114089.
XX PR 08-JUL-1999; 99JP-00194486.
XX PR 11-JAN-2000; 2000JP-00118774.
XX PR 02-MAY-2000; 2000JP-00183765.
XX PA (HELI-) HELIX RES INST.
XX PA
XX
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PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX N-PSDB; AAK94119.
DR WPI; 2001-524355/58.
XX 830 Primers useful for synthesizing full length cDNA clones and their use
XX PT in genetic manipulation.
XX PS Claim 8; SEQ ID NO 2608; 1380pp + Sequence Listing; English.
XX CC The invention relates to primers for synthesising full length cDNA
XX CC clones. 830 cDNA molecules encoding a human protein have been isolated
XX CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
XX CC been determined. Primers for synthesising the full length cDNA are useful
XX CC for clarifying the function of the protein encoded by the cDNA. The full
XX CC length clones were obtained by construction of full length enriched cDNA
XX CC libraries that were synthesised by the oligo-capping method. The primers
XX CC enable the production of the full length cDNA easily without any special
XX CC methods. The present sequence is a polypeptide encoded by a full length
XX CC human cDNA of the invention. Note: The sequence data for this patent did
XX CC not form part of the printed specification, but was obtained in CD-ROM
XX CC format directly from EPO
XX SQ Sequence 145 AA;

Query Match 16.7%; Score 88.5; DB 4; Length 145;
Best Local Similarity 30.7%; Pred. No. 0.045;
Matches 23; Conservative 6; Mismatches 13; Indels 33; Gaps 3;

QY 28 SPRSNSHSHPNPL-----KLHRRGSHSHNRPRAYILITILPSKLRTHSQSHHN- 76
Db 65 TPSSHPQHHTTYTTPSTPLNLRHRRPHSHPR-----LHTTRPHHL 109

QY 77 -----PLSRTSNS 84
Db 110 PRVRTAAPLHRPENS 124

Search completed: October 11, 2005, 07:11:09
Job time : 74.5829 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:16 ; Search time 164.294 Seconds
(without alignments)
248.149 Million cell updates/sec

Title: US-10-092-934-6

Perfect score: 531

Sequence: 1 EAYTLMHLPTNRPKIAHC.....SRTSNSTPTNSFLMTSSKPR 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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22:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	531	100.0	98	14	US-10-138-516-5
2	531	100.0	98	14	US-10-146-130-7
3	531	100.0	98	14	US-10-092-934-6
4	531	100.0	98	14	US-10-153-334-6
5	531	100.0	98	14	US-10-198-069-6
6	531	100.0	98	14	US-10-198-070-6
7	531	100.0	98	14	US-10-294-891-4
8	531	100.0	98	17	US-10-920-313-4
9	117	22.0	23	14	US-10-294-891-35
10	117	22.0	23	17	US-10-920-313-35
11	99.5	18.7	123	16	US-10-425-115-365713
Sequence 5, Appli					
Sequence 7, Appli					
Sequence 6, Appli					
Sequence 6, Appli					
Sequence 6, Appli					
Sequence 4, Appli					
Sequence 35, Appli					
Sequence 35, Appli					

12	90.5	17.0	117	16	US-10-437-963-165665	Sequence 165665,
13	90	16.9	136	15	US-10-424-599-177792	Sequence 177792,
14	89.5	16.9	185	13	US-10-835-121	Sequence 121, App
15	88	16.6	151	18	US-10-450-763-59813	Sequence 59813, A
16	88	16.6	400	14	US-10-301-822-155	Sequence 155, App
17	88	16.6	400	16	US-10-723-860-1111	Sequence 1111, Ap
18	88	16.6	400	16	US-10-370-7158-550	Sequence 550, App
19	88	16.6	400	18	US-10-970-698A-28	Sequence 28, Appl
20	86.5	16.3	682	18	US-10-450-763-34143	Sequence 34143, A
21	86	16.2	15	14	US-10-294-891-31	Sequence 31, Appl
22	86	16.2	15	17	US-10-920-313-31	Sequence 31, Appl
23	85.5	16.1	2958	20	US-11-097-143-40896	Sequence 40896, A
24	85	16.0	15	14	US-10-294-891-32	Sequence 32, Appl
25	85	16.0	15	17	US-10-920-313-32	Sequence 32, Appl
26	85	16.0	793	20	US-11-097-143-41856	Sequence 41856, A
27	84	15.8	15	14	US-10-294-891-30	Sequence 30, Appl
28	84	15.8	15	17	US-10-920-313-30	Sequence 30, Appl
29	83.5	15.7	273	9	US-09-764-864-1421	Sequence 1421, Ap
30	83.5	15.7	316	9	US-09-764-864-1036	Sequence 1036, Ap
31	83.5	15.7	720	15	US-10-200-012-18	Sequence 18, Appl
32	83	15.6	708	20	US-11-097-143-10932	Sequence 10932, A
33	82.5	15.5	207	15	US-10-424-599-283755	Sequence 283755,
34	82.5	15.5	226	15	US-10-108-260A-4030	Sequence 4030, Ap
35	81.5	15.3	657	17	US-10-794-514A-324	Sequence 324, App
36	81.5	15.3	1399	20	US-11-097-143-34929	Sequence 34929, A
37	81	15.3	261	14	US-10-280-953-17	Sequence 17, Appl
38	80	15.1	15	14	US-10-294-891-34	Sequence 34, Appl
39	80	15.1	15	17	US-10-920-313-34	Sequence 34, Appl
40	80	15.1	260	15	US-10-094-749-1890	Sequence 1890, Ap
41	79.5	15.0	67	16	US-10-425-115-310747	Sequence 310747,
42	79.5	15.0	1113	16	US-10-739-930-5799	Sequence 5799, Ap
43	79.5	15.0	3972	14	US-10-156-761-8476	Sequence 8476, Ap
44	79.5	15.0	3972	16	US-10-204-862A-4	Sequence 4, Appli
45	79.5	15.0	3972	16	US-10-204-862A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-10-138-516-5
; Sequence 5, Application US/10138516
; Publication No. US20030003445A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING ANTIBODIES TO
; TITLE OF INVENTION: NEURAL THREAD PROTEINS
; FILE REFERENCE: 59003.000004
; CURRENT APPLICATION NUMBER: US/10/138,516
; CURRENT FILING DATE: 2002-07-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-516-5

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Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-146-130-7

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; Sequence 7, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-7

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Best Local Similarity 100.0%; Pred. No. 8.7e-49;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-10-092-934-6
; Sequence 6, Application US/10092934
; Publication No. US20030054990A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHODS OF USING NEURAL THREAD PROTEINS TO TREAT TUMORS
; TITLE OF INVENTION: AND CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; FILE REFERENCE: 018792-0199
; CURRENT APPLICATION NUMBER: US/10/092,934
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/273,957
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Neural thread
US-10-092-934-6

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Best Local Similarity 100.0%; Pred. No. 8.7e-49;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-153-334-6
; Sequence 6, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; FILE REFERENCE: 59003-000006
; CURRENT APPLICATION NUMBER: US/10/153,334
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,156
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 98
; TYPE: PRT
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US-10-153-334-6

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US-10-198-069-6
; Sequence 6, Application US/10198069
; Publication No. US20030096756A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; FILE REFERENCE: 59003.000009
; CURRENT APPLICATION NUMBER: US/10/198,069
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown NTP
US-10-198-069-6

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Best Local Similarity 100.0%; Pred. No. 8.7e-49;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 LPSKLLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
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; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; FILE REFERENCE: 59003.000009
; CURRENT APPLICATION NUMBER: US/10/198,069
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
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; FEATURE:
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US-10-198-069-6

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; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 6
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Unknown NTP
; OTHER INFORMATION: peptide
US-10-198-070-6
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Best Local Similarity 100.0%; Pred. No. 8.7e-49;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 EAYTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHNRPRAYILITI 60
Qy 61 LPSKCLKRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
Db 61 LPSKCLKRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
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US-10-294-891-4
; Sequence 4, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-4
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Best Local Similarity 100.0%; Pred. No. 8.7e-49;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 EAYTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHNRPRAYILITI 60
Qy 61 LPSKCLKRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
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US-10-920-313-4
; Sequence 4, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
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; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
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Best Local Similarity 100.0%; Pred. No. 8.7e-49;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 EAYTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHNRPRAYILITI 60
Qy 61 LPSKCLKRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
Db 61 LPSKCLKRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
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US-10-294-891-35
; Sequence 35, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-35
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Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 76 NPLSRSTNSPTNSFLMTSSKPR 98
Db 1 NPLSRSTNSPTNSFLMTSSKPR 23
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US-10-920-313-35
; Sequence 35, Application US/10920313

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; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-35

Query Match      22.0%; Score 117; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      76 NPLSRSTNSPTNSFLMTSSKPR 98
Db      1 NPLSRSTNSPTNSFLMTSSKPR 23

RESULT 11
US-10-425-115-365713
; Sequence 365713, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 365713
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(123)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_96695C.1.pap
US-10-425-115-365713

Query Match      18.7%; Score 99.5; DB 16; Length 123;
Best Local Similarity 31.2%; Pred. No. 0.0096;
Matches 35; Conservative 13; Mismatches 43; Indels 21; Gaps 8;

QY      3 YVTMLH--LPTTRPKIAHCILFNQPHSPRSNSHSHPNPLKLH--RRSHSHN-----RPR 53
Db      4 YVTLLHTLTPXXHK-KSNH--TXSQHXAHSXSHXHXHTNKHSHXHTKHNLHLHXXHPH 60

QY      54 AYILITILPSKLRTHSQSHHN-PLSR-----TSNSTPTNSFLMTSSKP 97
Db      61 YXXLI-YHPXLTPIRHQTPSHHQPLSHYVYXHHSSISSTTILSYILYTPP 111

RESULT 12
US-10-437-963-165665
; Sequence 165665, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 165665
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_6444C.1.pap
US-10-437-963-165665

Query Match      17.0%; Score 90.5; DB 16; Length 117;
Best Local Similarity 27.6%; Pred. No. 0.082;
Matches 32; Conservative 10; Mismatches 51; Indels 23; Gaps 3;

QY      3 YVTMLHLPTRPKIAHCILFNQPHSPRSNSHSHPNPLKL-----HRRSHS-----HNR 51
Db      2 YHTQHTHTHTHTHTTTTFNFYVHTNSLSLTHSTNSLSLTHHTQTHSLSLTH 61

QY      52 PRAYLITILPSKLRTHSQSHHNPLS-----RTSNSTPTNSFLMTSS 95
Db      62 THNFTLTLLKKMHTKSLSTHTHTNPLSLSLSLSHHTHTQTHHTHTTNNFTHTST 117

RESULT 13
US-10-424-599-177792
; Sequence 177792, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 177792
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(136)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_131562C.1.pap
US-10-424-599-177792

Query Match      16.9%; Score 90; DB 15; Length 136;
Best Local Similarity 28.0%; Pred. No. 0.11;
Matches 26; Conservative 9; Mismatches 30; Indels 28; Gaps 5;

QY      5 TMLHLPTRPKIAHCILFNQPHS-----PRNSHSHPNPLK-----LHRRSHSHNRPR 53
Db      43 TLIHVP-----PHSTTIFHTNNHTHTPTSTTHHPPPLHHHPAPCILHLHHHT--- 92

QY      54 AYILITILPSKLRTHSQSHHNPLSRSTNSSTP 86
Db      93 -----YYXTPANPTTHHHHHPP--APANATP 118
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Db 78 APRSHSH-RPRR-----PTATWATHANSQPSTHKTGAGFLTLSTLQFRSGP 126

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Job time : 164.294 secs

RESULT 14
US-10-001-835-121
; Sequence 121, Application US/10001835
; Publication No. US20020160387A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Caferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro
; FILE REFERENCE: DEX-0277
; CURRENT APPLICATION NUMBER: US/10/001,835
; CURRENT FILING DATE: 2001-11-20
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/249,997
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 121
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-835-121

Query Match 16.9%; Score 89.5; DB 13; Length 185;
Best Local Similarity 33.0%; Pred. No. 0.18;
Matches 30; Conservative 15; Mismatches 33; Indels 13; Gaps 6;
Qy 4 YTMHLHTTNRPKTAHCILFNQPHSPR--SNSHSHNPPLKLRHRR-SHSHNRPRAYILITI 60
Db 100 HTSPHSPTYNH--LSHIFLNPQPPHHRLDSSPTHP-PLHIKQINHTSAPHNTHTRSTL 156
Qy 61 LPSKLRTHSQSHHNPRLSRTSNSTPTNSFL 91
Db 157 TTPPTTL--HSHSHSPL-----TTPHHLL 180

RESULT 15
US-10-450-763-59813
; Sequence 59813, Application US/10450763
; Publication No. US20050198754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIE3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 59813
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-59813

Query Match 16.6%; Score 88; DB 18; Length 151;
Best Local Similarity 31.6%; Pred. No. 0.2;
Matches 37; Conservative 9; Mismatches 37; Indels 34; Gaps 8;
Qy 4 YTMHL-----PTTNRPK--IAHCILFNQPHSPRNS-----HSHNPPL---KL 42
Db 21 HTVLTHAKSHIHFGTRSPNHTVTGC---PHPTQGRSSRTHTPPSAHSHKRPDLHPES 77
Qy 43 HRRSHSHNRPRAYILITILPSKLRTHSQSHHNPRLS--RTSNSTPTNSFLMTSSKP 97

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:19 ; Search time 22.4037 Seconds
(without alignment)
326.535 Million cell updates/sec

Title: US-10-092-934-6

Perfect score: 531

Sequence: 1 EAYTLMHLPTNRPKIAHC.....SRTSNSTPTNSFLMTSSKPR 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap:*
 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap:*
 - 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap:*
 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap:*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pap:*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	531	100.0	98	2	US-08-454-557C-30
2	531	100.0	98	2	US-08-340-426D-30
3	531	100.0	98	2	US-08-450-673C-30
4	531	100.0	98	5	PCT-US95-17111A-30
5	81	15.3	261	4	US-09-602-565-34
6	80.5	15.2	651	1	US-08-431-080-24
7	80.5	15.2	651	2	US-08-938-534-24
8	80.5	15.2	651	3	US-09-345-294-24
9	75.5	14.2	379	4	US-09-270-767-57074
10	75.5	14.2	1557	4	US-09-410-551B-27
11	75.5	14.2	1557	4	US-09-940-316B-27
12	75.5	14.2	1574	4	US-09-410-551B-25
13	75.5	14.2	1574	4	US-09-940-316B-25
14	75.5	14.2	1578	4	US-09-410-551B-31
15	75.5	14.2	1578	4	US-09-940-316B-31
16	75.5	14.2	1588	4	US-09-410-551B-29
17	75.5	14.2	1588	4	US-09-940-316B-29
18	75.5	14.2	1605	4	US-09-410-551B-33
19	75.5	14.2	1605	4	US-09-940-316B-33
20	75	14.1	165	4	US-03-252-931A-25261
21	75	14.1	170	4	US-09-270-767-44218
22	75	14.1	639	4	US-09-949-016-6812
23	75	14.1	652	4	US-09-949-016-7323
24	74.5	14.0	423	4	US-09-270-767-41561
25	74	13.9	254	4	US-09-248-796A-19089
26	74	13.9	834	2	US-08-861-464-4
27	74	13.9	834	2	US-08-396-001-4

28	74	13.9	834	3	US-09-323-433A-4	Sequence 4, Appli
29	74	13.9	834	4	US-09-826-752-4	Sequence 4, Appli
30	73.5	13.8	410	4	US-09-270-767-43824	Sequence 43824, A
31	73	13.7	1013	4	US-09-612-402B-15	Sequence 15, Appl
32	73	13.7	1013	4	US-09-612-402B-16	Sequence 16, Appl
33	72	13.6	544	4	US-09-532-594B-18	Sequence 18, Appl
34	72	13.6	598	4	US-09-532-594B-16	Sequence 16, Appl
35	72	13.6	734	4	US-09-532-594B-4	Sequence 4, Appli
36	71.5	13.5	1007	4	US-10-144-198-36	Sequence 36, Appl
37	71.5	13.5	1041	4	US-10-144-198-14	Sequence 14, Appl
38	71	13.4	668	1	US-08-468-036-5	Sequence 5, Appli
39	71	13.4	668	2	US-08-376-843-5	Sequence 5, Appli
40	71	13.4	668	4	US-09-538-092-19	Sequence 19, Appl
41	71	13.4	1482	4	US-09-410-551B-21	Sequence 21, Appl
42	71	13.4	1482	4	US-09-940-316B-21	Sequence 21, Appl
43	71	13.4	1488	4	US-09-410-551B-17	Sequence 17, Appl
44	71	13.4	1488	4	US-09-940-316B-17	Sequence 17, Appl
45	71	13.4	1509	4	US-09-410-551B-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-454-557C-30
; Sequence 30, Application US/08454557C
; Patent No. 5830670
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,557C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-454-557C-30

Query Match 100.0%; Score 531; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2e-55;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EAYTLMHLPTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRSNRPAYILITI 60
Db 1 EAYTLMHLPTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRSNRPAYILITI 60
Qy 61 LPSKLKLRTHSQSHNPLSRITSNSTPTNSFLMTSSKPR 98

Db 61 LPSKCLKLRTHSQSHHNPLSRSTNSPTNSFLMTSSKPR 98

RESULT 2

US-08-340-426D-30

Sequence 30, Application US/08340426D

Patent No. 5948634

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

APPLICANT: Wands, Jack R.

TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection

TITLE OF INVENTION: of Alzheimer's Disease

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/340,426D

FILING DATE: 14-NOV-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0609.3840002

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-340-426D-30

Query Match 100.0%; Score 531; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 2e-55;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 EAYYTMHLPTNRPKIAHCILFNQPHSPRNSHSHNPPLKLRHRRSHHNPRAVYILITI 60

Qy 61 LPSKCLKLRTHSQSHHNPLSRSTNSPTNSFLMTSSKPR 98

Db 61 LPSKCLKLRTHSQSHHNPLSRSTNSPTNSFLMTSSKPR 98

RESULT 3

US-08-450-673C-30

Sequence 30, Application US/08450673C

Patent No. 5948888

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

APPLICANT: Wands, Jack R.

TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection

TITLE OF INVENTION: of Alzheimer's Disease

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,673C

FILING DATE: 30-MAY-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0609.3840004

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-450-673C-30

Query Match 100.0%; Score 531; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 2e-55;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EAYYTMHLPTNRPKIAHCILFNQPHSPRNSHSHNPPLKLRHRRSHHNPRAVYILITI 60

Db 1 EAYYTMHLPTNRPKIAHCILFNQPHSPRNSHSHNPPLKLRHRRSHHNPRAVYILITI 60

Qy 61 LPSKCLKLRTHSQSHHNPLSRSTNSPTNSFLMTSSKPR 98

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,673C

FILING DATE: 30-MAY-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0609.3840004

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-450-673C-30

Query Match 100.0%; Score 531; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 2e-55;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 EAYYTMHLPTNRPKIAHCILFNQPHSPRNSHSHNPPLKLRHRRSHHNPRAVYILITI 60

Qy 61 LPSKCLKLRTHSQSHHNPLSRSTNSPTNSFLMTSSKPR 98

Db 61 LPSKCLKLRTHSQSHHNPLSRSTNSPTNSFLMTSSKPR 98

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

APPLICANT: Wands, Jack R.

TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection

TITLE OF INVENTION: of Alzheimer's Disease

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,673C

FILING DATE: 30-MAY-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0609.3840004

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-450-673C-30

Query Match 100.0%; Score 531; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 2e-55;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EAYYTMHLPTNRPKIAHCILFNQPHSPRNSHSHNPPLKLRHRRSHHNPRAVYILITI 60

Db 1 EAYYTMHLPTNRPKIAHCILFNQPHSPRNSHSHNPPLKLRHRRSHHNPRAVYILITI 60

Qy 61 LPSKCLKLRTHSQSHHNPLSRSTNSPTNSFLMTSSKPR 98

Db 61 LPSKCLKLRTHSQSHHNPLSRSTNSPTNSFLMTSSKPR 98

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

APPLICANT: Wands, Jack R.

TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection

TITLE OF INVENTION: of Alzheimer's Disease

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,673C

FILING DATE: 30-MAY-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0609.3840004

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-450-673C-30

Query Match 100.0%; Score 531; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 2e-55;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 EAYYTMHLPTNRPKIAHCILFNQPHSPRNSHSHNPPLKLRHRRSHHNPRAVYILITI 60

Qy 61 LPSKCLKLRTHSQSHHNPLSRSTNSPTNSFLMTSSKPR 98

Db 61 LPSKCLKLRTHSQSHHNPLSRSTNSPTNSFLMTSSKPR 98

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

APPLICANT: Wands, Jack R.

TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection

TITLE OF INVENTION: of Alzheimer's Disease

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,673C

FILING DATE: 30-MAY-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0609.3840004

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540</

```
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US95-17111A-30

Query Match 100.0%; Score 531; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 2e-55;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EAYTMLHLPTTNRPKIAHCILFNQPHSRNSHSHNPPLKLRSHSHNRPRAYILITI 60
   |||||
Db 1 EAYTMLHLPTTNRPKIAHCILFNQPHSRNSHSHNPPLKLRSHSHNRPRAYILITI 60

Qy 61 LPSKLRTHSQSHHNPPLSTNSPTNSFLMTSSKPR 98
   |||||
Db 61 LPSKLRTHSQSHHNPPLSTNSPTNSFLMTSSKPR 98

RESULT 5
US-09-602-565-34
; Sequence 34, Application US/09602565
; Patent No. 6500642
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Patterson, Chandra
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: MOLECULE ASSOCIATED WITH APOPTOSIS
; FILE REFERENCE: PC-0018 US
; CURRENT APPLICATION NUMBER: US/09/602,565
; CURRENT FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/106,120
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PERL Program
; SEQ ID NO 34
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6500642 g1469400
US-09-602-565-34

Query Match 15.3%; Score 81; DB 4; Length 261;
Best Local Similarity 34.7%; Pred. No. 0.12;
Matches 25; Conservative 4; Mismatches 33; Indels 10; Gaps 4;

Qy 14 RPKIAHCILFNQPHSRNSHSHNPPLKLRSHSHNRPRAYILITILPSKLRTHSQS 73
   |||||
Db 198 QPQQLHSYPPHPH-PYSHPHQHPH---HPHPHPHPHPYQL-----QHAHQPLHSQP 248

Qy 74 H-HNPLSRSTNS 84
   |||||
Db 249 QGHRLLRSTNS 260

RESULT 6
US-08-431-080-24
; Sequence 24, Application US/08431080
; Patent No. 5698686
; GENERAL INFORMATION:
; APPLICANT: Gottschling, Daniel E.
; APPLICANT: Singer, Miriam S.
; TITLE OF INVENTION: Telomerase Compositions and Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,080
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SN 08/326,781
FILING DATE: October 20, 1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-431-080-24

Query Match 15.2%; Score 80.5; DB 1; Length 651;
Best Local Similarity 29.1%; Pred. No. 0.43;
Matches 25; Conservative 14; Mismatches 34; Indels 13; Gaps 2;

Qy 26 PHSPRSNSHSHNPPLKLRSHSHNRPRAYILITILPS-----KLRTHSQSHH 75
   |||||
Db 206 PHHPQHLLHHHPHKTLPKPSNSHSTNSLNQDPVRSNDEEKYGFIPKVFVRSRSSFA 265

Qy 76 NPLS---RTSNSTPTNSFLMTSSKPR 98
   |||||
Db 266 YPQQVAITTTSPSPNSHVLSSKSR 291

RESULT 7
US-08-938-534-24
; Sequence 24, Application US/08938534
; Patent No. 5916752
; GENERAL INFORMATION:
; APPLICANT: Gottschling, Daniel E.
; APPLICANT: Singer, Miriam S.
; TITLE OF INVENTION: Telomerase Compositions and Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,534
FILING DATE: 26-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,080
FILING DATE:
APPLICATION NUMBER: SN 08/326,781
FILING DATE: October 20, 1994
ATTORNEY/AGENT INFORMATION:
```



```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
; OTHER INFORMATION: synthase fragment
US-09-410-551B-27

Query Match      14.2%; Score 75.5; DB 4; Length 1557;
Best Local Similarity 26.3%; Pred. No. 5;
Matches 25; Conservative 12; Mismatches 43; Indels 15; Gaps 3;

Qy 8 HLPITNRPKIAHCILFNQPHS-----PRSNHSHPNPKLHRRSHSHNRPRAYILITILP 62
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1271 HLITTNHTLVHTTT-DPPGAAVTGLTRTAQNEHPGRIHLIETHHPHTPLPLTQLTTLHQ 1329
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 63 SKLKLRTHS-----QSHHNPLSRTSNSTPTN 88
    || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1330 PHLRLTNTLHTPLHTPIITTHNTTTTTPPTPLN 1364

RESULT 11
US-09-940-316B-27
; Sequence 27, Application US/09940316B
; Patent No. 6759536
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDES ENCODING THE FKBA GENE OF THE FK-520 POLYKETIDE SYNTH
; FILE REFERENCE: 30062-20026.11
; CURRENT APPLICATION NUMBER: US/09/940,316B
; CURRENT FILING DATE: 2001-08-27
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1557
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
; OTHER INFORMATION: synthase fragment
US-09-940-316B-27

Query Match      14.2%; Score 75.5; DB 4; Length 1557;
Best Local Similarity 26.3%; Pred. No. 5;
Matches 25; Conservative 12; Mismatches 43; Indels 15; Gaps 3;

Qy 8 HLPITNRPKIAHCILFNQPHS-----PRSNHSHPNPKLHRRSHSHNRPRAYILITILP 62
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1271 HLITTNHTLVHTTT-DPPGAAVTGLTRTAQNEHPGRIHLIETHHPHTPLPLTQLTTLHQ 1329
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 63 SKLKLRTHS-----QSHHNPLSRTSNSTPTN 88
    || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1330 PHLRLTNTLHTPLHTPIITTHNTTTTTPPTPLN 1364

RESULT 12
US-09-410-551B-25
; Sequence 25, Application US/09410551B
; Patent No. 6503737
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDES ENCODING THE FKBA GENE OF THE FK-520 POLYKETIDE SYNTH
; FILE REFERENCE: 30062-20026.11
; CURRENT APPLICATION NUMBER: US/09/940,316B
; CURRENT FILING DATE: 2001-08-27
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1557
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
; OTHER INFORMATION: synthase fragment
US-09-940-316B-27

Query Match      14.2%; Score 75.5; DB 4; Length 1557;
Best Local Similarity 26.3%; Pred. No. 5;
Matches 25; Conservative 12; Mismatches 43; Indels 15; Gaps 3;

Qy 8 HLPITNRPKIAHCILFNQPHS-----PRSNHSHPNPKLHRRSHSHNRPRAYILITILP 62
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1271 HLITTNHTLVHTTT-DPPGAAVTGLTRTAQNEHPGRIHLIETHHPHTPLPLTQLTTLHQ 1329
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 63 SKLKLRTHS-----QSHHNPLSRTSNSTPTN 88
    || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1330 PHLRLTNTLHTPLHTPIITTHNTTTTTPPTPLN 1364

RESULT 13
US-09-940-316B-25
; Sequence 25, Application US/09940316B
; Patent No. 6759536
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDES ENCODING THE FKBA GENE OF THE FK-520 POLYKETIDE SYNTH
; FILE REFERENCE: 30062-20026.11
; CURRENT APPLICATION NUMBER: US/09/940,316B
; CURRENT FILING DATE: 2001-08-27
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
; OTHER INFORMATION: synthase fragment
US-09-410-551B-25

Query Match      14.2%; Score 75.5; DB 4; Length 1574;
Best Local Similarity 26.3%; Pred. No. 5.1;
Matches 25; Conservative 12; Mismatches 43; Indels 15; Gaps 3;

Qy 8 HLPITNRPKIAHCILFNQPHS-----PRSNHSHPNPKLHRRSHSHNRPRAYILITILP 62
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1288 HLITTNHTLVHTTT-DPPGAAVTGLTRTAQNEHPGRIHLIETHHPHTPLPLTQLTTLHQ 1346
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 63 SKLKLRTHS-----QSHHNPLSRTSNSTPTN 88
    || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1347 PHLRLTNTLHTPLHTPIITTHNTTTTTPPTPLN 1381

RESULT 14
US-09-940-316B-25
; Sequence 25, Application US/09940316B
; Patent No. 6759536
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDES ENCODING THE FKBA GENE OF THE FK-520 POLYKETIDE SYNTH
; FILE REFERENCE: 30062-20026.11
; CURRENT APPLICATION NUMBER: US/09/940,316B
; CURRENT FILING DATE: 2001-08-27
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
; OTHER INFORMATION: synthase fragment
US-09-410-551B-25
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 11.631 Seconds
(without alignments)
620.432 Million cell updates/sec

Title: US-10-092-934-7
Perfect score: 409
Sequence: 1 SSSLGPKCWDYRHLLSLA.....CPVKIALLTINGHCTWLPAS 75

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: Piri.*
2: Piri2.*
3: Piri3.*
4: Piri4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73	17.8	252	2 PC4259	ferritin associate
2	73	17.8	627	4 A40201	artifact-warning s
3	68	16.6	613	4 C40201	artifact-warning s
4	65	15.9	597	4 E40201	artifact-warning s
5	62.5	15.3	191	1 W6WLK1	E6 protein - rhesu
6	62.5	15.3	346	2 T47411	hypothetical prote
7	60.5	14.8	2946	2 T15840	hypothetical prote
8	60	14.7	1808	2 T47792	hypothetical prote
9	59	14.4	569	2 B84470	Mutator-like trans
10	59	14.4	951	2 T00017	gene ADAMTS-1 prot
11	58	14.2	301	4 B40201	artifact-warning s
12	58	14.2	1628	2 T43682	nucleoporin - fiss
13	57	13.9	442	2 T42955	hypothetical prote
14	57	13.9	734	2 T02196	hypothetical prote
15	57	13.9	882	2 T01168	hypothetical prote
16	56.5	13.8	118	2 G90129	hypothetical prote
17	56.5	13.8	139	2 G97240	amino acid transpo
18	56.5	13.8	185	1 J02394	phospholipase A2 i
19	56.5	13.8	355	2 J42397	opsin, green-sensi
20	56.5	13.8	498	1 HJBE11	helicase (EC 3.6.1
21	56.5	13.8	727	2 A71069	hypothetical prote
22	56	13.7	276	2 T49123	hypothetical prote
23	56	13.7	535	2 S48268	probable membrane
24	56	13.7	564	2 T41168	hypothetical prote
25	56	13.7	682	2 T41680	hypothetical prote
26	55.5	13.6	151	2 E43584	15K cysteine-rich
27	55.5	13.6	349	2 B45229	opsin, green-sensi
28	55	13.4	150	2 C71515	probable 15kDa cys
29	55	13.4	152	2 F43584	15K cysteine-rich

30 55 13.4 316 2 T21039
31 55 13.4 354 2 J04152
32 55 13.4 354 2 S34378
33 55 13.4 490 2 T46162
34 55 13.4 521 2 T46250
35 55 13.4 673 4 F40201
36 55 13.4 843 2 H82362
37 54.5 13.3 220 2 T28503
38 54.5 13.3 220 2 S33080
39 54.5 13.3 220 2 G72158
40 54.5 13.3 259 2 T23849
41 54.5 13.3 428 2 B84964
42 54.5 13.3 458 2 A29361
43 54.5 13.3 519 2 AH0064
44 54.5 13.3 639 2 T31983
45 54.5 13.3 822 1 TVHUFE

hypothetical prote
wnt-11 protein pre
wnt-11 protein - m
glucosyltransferas
hypothetical prote
artifact-warning s
adenylate cyclase
hypothetical prote
G2R protein - vari
f3R protein - vari
adenosylmethionine
hypothetical prote
DG17 protein - sli
thiamin transport
hypothetical prote
protein-tyrosine k

ALIGNMENTS

RESULT 1

PC4259
ferritin associated protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: PC4259
R;Kedar, V.; Moss, D.; Halliday, J.; Powell, L.
Biochem. Biophys. Res. Commun. 228, 683-689, 1996
A;Title: Molecular cloning of a partial cDNA of a novel gene in iron metabolism.
A;Reference number: PC4259; MUID:97096315; PMID:8941339
A;Accession: PC4259
A;Molecule type: mRNA
A;Residues: 1-252 <KED>
A;Cross-references: UNIPROT:P78394; GB:U63542; NID:g1890646; PIDN:AAC51145.1; PID:g18906
A;Experimental source: T lymphoid cell
C;Comment: This protein plays roles in normal cellular iron metabolism and in iron overl.

Query Match 17.8%; Score 73; DB 2; Length 252;
Best Local Similarity 40.4%; Pred. No. 0.21;
Matches 19; Conservative 2; Mismatches 14; Indels 12; Gaps 2;

Qy 1 SSSLGPKCWDYR-----HELLSLALMINFR-VMACTFKQH 35
Db 20 SSSLGLPKCWDYRGDPPRPVLEDGSESLEYLSSNLKEVLACRGLSH 66

RESULT 2

A40201
artifact-warning sequence (translated ALU class A) - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C;Accession: A40201
R;Claverie, J.M.
Personal communication, 1992
A;Reference number: A40201
A;Accession: A40201
A;Molecule type: DNA
A;Residues: 1-627 <CLA>
R;Claverie, J.M.
Genomics 12, 838-841, 1992
A;Title: Identifying coding exons by similarity search: Alu-derived and other potentiall
A;Reference number: A40200; MUID:92241891; PMID:1572661
A;Contents: annotation
C;Comment: This "warning" entry is a conceptual translation in all 6 reading frames of o
in-frame stop codons are shown as 'X'.
C;Comment: Any significant similarity of a predicted protein sequence to a portion of th

Query Match 17.8%; Score 73; DB 4; Length 627;
Best Local Similarity 80.0%; Pred. No. 0.5;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 386 CVDETCPW 393

RESULT 10

T00017

gene ADAMTS-1 protein - mouse

C;Species: Mus musculus (house mouse)

C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 15-Mar-2004

C;Accession: T00017

R;Kuno, K.; Lizasa, H.; Ohno, S.; Matsushima, K.

Genomics 46, 466-471, 1997

A;Title: The exon/intron organization and chromosomal mapping of the mouse ADAMTS-1

A;Reference number: Z14055; MUID:98110583; PMID:9441751

A;Accession: T00017

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-951 <KUN>

A;Cross-references: EMBL:AB001735; NID:92809056; PIDN:BA24501.1; PID:92809057

A;Experimental source: strain 129SVJ

C;Genetics:

A;Gene: ADAMTS-1

A;Introns: 228/1; 343/3; 388/1; 444/1; 539/3; 602/1; 660/3; 719/2

F;542-598/Domain: thrombospondin type 1 repeat homology <THR>

Query Match 14.4%; Score 59; DB 2; Length 951;

Best Local Similarity 32.8%; Pred. No. 39;

Matches 21; Conservative 8; Mismatches 23; Indels 12; Gaps 4;

QY 13 RHELLSLALMINFRVMACTFKQHIETROKTSIVPRKLCM-----GPVCPVKIALTLTG 67

DB 263 KHYLLTL-----FSV-AARFKHPSIRNSISLVVVKILVIEYEQKGPEV-TSNAALTLRN 315

QY 68 HCTW 71

DB 316 FCNW 319

RESULT 11

B40201

artifact-warning sequence (translated ALU class B) - human

C;Species: Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000

C;Accession: B40201

R;Claverie, J.M.

personal Communication, 1992

A;Reference number: A40201

A;Accession: B40201

A;Molecule type: DNA

A;Residues: 1-301 <CLA>

R;Claverie, J.M.

Genomics 12, 838-841, 1992

A;Title: Identifying coding exons by similarity search: Alu-derived and other p

A;Reference number: A40200; MUID:92241891; PMID:1572661

A;Contents: annotation

C;Comment: This "warning" entry is a conceptual translation in all 6 reading fr

in-frame stop codons are shown as 'X'.

C;Comment: Any significant similarity of a predicted protein sequence to a port

Query Match 14.2%; Score 58; DB 4; Length 301;

Best Local Similarity 69.2%; Pred. No. 18;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SSSLGLPKCWDYR 13

DB 232 SSYFSIPKCWDYR 244

RESULT 12

T43682

nucleoporin - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text change 21-Jul-2000

C;Accession: T43682
R;Whalen, W.A.; Yoon, J.H.; Shen, R.; Dhar, R.
Genetics 152, 827-838, 1999
A;Title: Regulation of mRNA export by nutritional status in fission yeast.
A;Reference number: 222629; MUID:99318821; PMID:10388805
A;Accession: T43682
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1628 <WHA>
A;Cross-references: EMBL:AF050355; NID:G5478223; PIDN:AAD43830.1; PID:G5478224
A;Experimental source: strain 972
C;Genetics:
A;Gene: nup184
A;Introns: 6/2

Query Match 14.2%; Score 58; DB 2; Length 1628;
Best Local Similarity 23.9%; Pred. No. 86;
Matches 22; Conservative 10; Mismatches 20; Indels 40; Gaps 3;

QY 12 YRHLSLALMINF-----RVMA-----CTFKQHIELROKISI----- 44
Db 815 YLHPLLSVMDLINLLYTDIFSTISSPRAKAKWMLISSFCAMKTLICLRGFLNLKPSLE 874
QY 45 -----VPRKLCMGVPCVPVKIAL 63
Db 875 RELFSRSPDLFNCLPRLCCIAPIQLLSALI 906

RESULT 13
T42955
hypothetical protein 40 - ateline herpesvirus 3 (strain 73)
C;Species: ateline herpesvirus 3
A;Variety: strain 73
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42955
R;Albrecht, J.C.; Fleckenstein, B.
submitted to the EMBL Data Library, August 1998
A;Description: Primary structure of the herpesvirus ateles genome.
A;Reference number: 222274
A;Accession: T42955
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-442 <ALB>
A;Cross-references: UNIPROT:Q9VTM5; EMBL:AF083424; PIDN:AAC95566.1
A;Experimental source: strain 73
C;Superfamily: ateline herpesvirus 3 hypothetical protein 40

Query Match 13.9%; Score 57; DB 2; Length 442;
Best Local Similarity 28.9%; Pred. No. 34;
Matches 22; Conservative 6; Mismatches 26; Indels 22; Gaps 3;

QY 3 SLGLPKCWDYRHLLSLALMIN---FRVMACTF---KQHIELROKISIVPRKLCMGVPV 55
Db 174 SEGLYRCSATREPPLKKTQOINIEDLFKINCFSFVAKIHINVRTIPI----- 222
QY 56 CPVKIALLLINGHCTW 71
Db 223 -----FHLWVNVCKW 234

RESULT 14
T02196
hypothetical protein At2g46910 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F14M4.26
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Ron
submitted to the EMBL Data Library, September 1998
A;Description: Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence.
A;Reference number: Z14609
A;Accession: T02196
A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-734 <ROU>
A;Cross-references: UNIPROT:O80733; EMBL:AC004411; NID:G3522932; PID:G3522947
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84908
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-734 <STO>
A;Cross-references: GB:AE002093; NID:G3522947; PIDN:AAC34229.1; GSPDB:GN00139
C;Genetics:
A;Gene: F14M4.26; At2g46910
A;Map position: 2
A;Introns: 138/2; 167/3; 214/2; 259/3; 369/2; 406/3; 467/2; 513/3; 535/3; 547/3; 560/1; 5
C;Superfamily: Arabidopsis thaliana hypothetical protein F14M4.26

Query Match 13.9%; Score 57; DB 2; Length 734;
Best Local Similarity 27.2%; Pred. No. 55;
Matches 22; Conservative 18; Mismatches 27; Indels 14; Gaps 5;

QY 4 LGLPKCWDYRHLLSLALMIN--FRVMACTFKQHIELROKISI---VPRKLCMGVPCP 57
Db 503 LGYKQTWD-RYQNMYSKGVGDRCFPMYDTFKIKVMRVEKAISTLTVP-KACCYRDTIG 560

QY 58 VKIAL-----LTINGHCTWL 72
Db 561 LEWSVEVLQDSMELSDCFWL 581

RESULT 15
T01168
hypothetical protein F7N22.13 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01168
R;Dante, M.
submitted to the EMBL Data Library, April 1998
A;Description: The sequence of A. thaliana F7N22.
A;Reference number: Z14250
A;Accession: T01168
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-882 <DAN>
A;Cross-references: UNIPROT:O65231; EMBL:AF058825; NID:G3047060; PID:G3047071
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 4
A;Introns: 60/1; 230/1; 852/3
A;Note: F7N22.13
C;Superfamily: Arabidopsis thaliana hypothetical protein F26C24.7

Query Match 13.9%; Score 57; DB 2; Length 882;
Best Local Similarity 23.5%; Pred. No. 65;
Matches 16; Conservative 11; Mismatches 23; Indels 18; Gaps 3;

QY 22 MINFRV-----MACTFKQHIELROKISIVPRKLC-C--MGVPCVPVKIAL 63
Db 289 LNFRADETQAEISTTCETLFGVGFKNRKVLQOTMSLQPIKQCFKQPKSCP KTLKMV 348
QY 64 TTINGHCTW 71
Db 349 CVDETCPW 356

Search completed: October 11, 2005, 07:01:39
Job time : 12.631 secs

OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC	TTSUB=Cerebellum;
RA	Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiayama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B., Nagai K., Isogai T., Sugano S.; Submitted (OCT-2001) to the ENBL/GenBank/DDJB databases. DR EMBL; AK057815; BABY1588.1; -; SQ SEQUENCE 160 AA; 18242 MW; 702C9970AA279A11 CRC64;
Query Match 21.3%; Score 87; DB 2; Length 160; Best Local Similarity 50.0%; Pred. No. 0.0081; Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;	
Qy	1 SSLSGLPKCWDIRHELSSLALMINFRVMAC 30 : : :: :: Dd 3 SPHYLPKCWNYRHEPLCLAVCFHFQLSLC 32
RESULT 3	
Q9PIY7	PRELIMINARY; PRT; 477 AA.
ID Q9PIY7	
AC Q9PIY7	
DT 01-OCT-2000	(TrEMBLrel. 15, Created)
DD 01-OCT-2000	(TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004	(TrEMBLrel. 26, Last annotation update)
DE KIAA1541 protein (fragment).	
GN Name=KIAA1541;	
GZ Homo sapiens (Human);	
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. ON NCBI_TaxID=9606; RX [1] SEQUENCE FROM N.A. MEDLINE=20277482; PubMed=10819331; RA Negase T., Kikumoto R., Ishikawa K., Hirosewa M., Ohara O.; RT "Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro"; RL DNA Res. 7:143-150(2000). CC -I- SIMILARITY: Contains 5 WD repeats. DR EMBL; AB040974; BAA96085.1; -. DR Genew; HGNC:23732; PPP2R2D. DR GO; GO:0000159; C:protein phosphatase type 2A complex; IEA. DR GO; GO:0008601; F:protein phosphatase type 2A regulator activity; IEA. DR GO; GO:0007165; P:signal transduction; IEA. DR InterPro; IPRO000009; PP2A_PR55. DR InterPro; IPRO01680; WD40. DR InterPro; IPRO11046; WD40_like. DR Pfam; PF00400; WD40; 5. DR PRINTS; PR00600; PP2APRS5. DR SMART; SM00320; WD40; 7. DR PROSITE; PS01024; PR55_1; 1. DR PROSITE; PS01025; PR55_2; 1. KW Repeat; WD repeat. FT NON TER 1 SQ SEQUENCE 477 AA; 55544 MW; B20AB833C6C5DFC9 CRC64;	
Query Match 21.0%; Score 86; DB 2; Length 477; Best Local Similarity 29.0%; Pred. No. 0.033; Matches 20; Conservative 13; Mismatches 24; Indels 12; Gaps 2;	
Qy	1 SSLSGLPKCWDIRHELSSLALMINFRVMACTFKOHIEL----PQKISIVPRKLCCMGVP 55 : : :: :: Dd 1 SSLHLGCPKEWKPEHPVAATCLFSLRVNWRSYRELGPLLSHTRALTFGH----- 53
Qy	56 CPVKIALLT 64 ::: Dd 54 CPLKSDIIIS 62
PRELIMINARY; PRT; 138 AA.	
RESULT 4	
Q6ZVL2	
ID Q6ZVL2	


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RESULT 6
Q6ZN97 Q6ZN97 PRELIMINARY; PRT; 134 AA.
AC Q6ZN97; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ16303.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Kanohori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
RA Tanai H., Watanabe S., Ishida S., Ono Y., Horita T., Watanabe M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Kugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK131315; BAD18478.1; -.
SQ SEQUENCE 134 AA; 15299 MW; A49A2899FB14AE2F CRC64;

Query Match 19.3%; Score 79; DB 2; Length 134;
Best Local Similarity 51.7%; Pred. No. 0.069;
Matches 15; Conservative 6; Mismatches 6; Indels 2; Gaps 1;

QY 4 LGLPKCDWYRHEHLSLA--LMINFRVNVAC 30
DB 100 LGLPKCDWYRCEPLHQLHQFVILNLFLLSC 128

RESULT 7
Q8NED3 Q8NED3 PRELIMINARY; PRT; 94 AA.
AC Q8NED3; 2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)."
```

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RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032019; AAH32019.1; -.
KW Hypothetical protein.
SQ SEQUENCE 94 AA; 11243 MW; DC87F1464046578C CRC64;

Query Match 19.1%; Score 78; DB 2; Length 94;
Best Local Similarity 66.7%; Pred. No. 0.064;
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 SSSIGLPKCDWYRHEHLSLA 21
DB 74 SACLGFPCWDYRSEPLRLAI 94

RESULT 8
ALU7_HUMAN ALU7_HUMAN STANDARD; PRT; 593 AA.
AC P39194;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alu subfamily SQ sequence contamination warning entry.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95021758; PubMed=7935834; DOI=10.1038/371752a0;
RA Claverie J.-M., Makalowski W.;
RT "Alu alert.";
RL Nature 371:752-752(1994).
RN [2]
RP CONCEPT.
RX MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.;
RT "Identifying coding exons by similarity search: alu-derived and other
RT potentially misleading protein sequences.";
RL Genomics 12:838-841(1992).
RN [3]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA Quentin Y.;
RT "The Alu family developed through successive waves of fixation closely
RT connected with primate lineage history.";
RL J. Mol. Evol. 27:194-202(1988).
RN [4]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J., Milosavljevic A.;
RT "Reconstruction and analysis of human Alu genes.";
RL J. Mol. Evol. 32:105-121(1991).
CC -1- MISCELLANEOUS: Various analyses indicate that Alu repeats fall
CC into 8 subfamilies (Ref.3 and Ref.4). Therefore, 8 Alu warning
CC consensus sequences have been constituted that contain all six
CC frames conceptual translations of each of these classes of Alu
CC repeats.
CC -1- MISCELLANEOUS: Isolated 'X' indicates the presence of a stop
CC codon, 'XXX' is used to separate the various translation phases.
CC -1- CAUTION: This Alu entry is provided in order to avoid the further
CC pollution of protein sequence databases with Alu-derived amino
CC acid sequences.
CC -1- CAUTION: Alu repetitive sequences are interspersed in human and
CC primate genomes with an average spacing of 4 kb. Some of them are
CC actively transcribed by pol III. Normal transcripts may contain
CC Alu-derived sequences in 5' or 3' untranslated regions. However,
CC cDNA libraries also contain partial and/or rearranged cDNAs
CC ligated with Alu-derived sequence in any orientation. Although Alu
CC elements (especially situated on the complementary strand) have a
```


RL Nature 371:752-752(1994).
RN [2]
RP CONCEPT.
RX MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.;
RT "Identifying coding exons by similarity search: alu-derived and other
RT potentially misleading protein sequences.";
RL Genomics 12:838-841(1992).
RN [3]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA Quentin Y.;
RT "The Alu family developed through successive waves of fixation closely
RT connected with primate lineage history.";
RL J. Mol. Evol. 27:194-202(1988).
RN [4]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J., Milosavljevic A.;
RT "Reconstruction and analysis of human Alu genes.";
RL J. Mol. Evol. 32:105-121(1991).
CC -!- MISCELLANEOUS: Various analyses indicate that Alu repeats fall
CC into 8 subfamilies (Ref.3 and Ref.4). Therefore, 8 Alu warning
CC consensus sequences have been constituted that contain all six
CC frames conceptual translations of each of these classes of Alu
CC repeats.
CC -!- MISCELLANEOUS: Isolated 'X' indicates the presence of a stop
CC codon, 'XXX' is used to separate the various translation phases.
CC -!- CAUTION: This Alu entry is provided in order to avoid the further
CC pollution of protein sequence databases with Alu-derived amino
CC acid sequences.
CC -!- CAUTION: Alu repetitive sequences are interspersed in human and
CC primate genomes with an average spacing of 4 kb. Some of them are
CC actively transcribed by pol III. Normal transcripts may contain
CC Alu-derived sequences in 5' or 3' untranslated regions. However,
CC cDNA libraries also contain partial and/or rearranged cDNAs
CC ligated with Alu-derived sequence in any orientation. Although Alu
CC elements (especially situated on the complementary strand) have a
CC great potential to create additional/alternative exons,
CC consideration should be given to the possibility that the presence
CC of an Alu in an open reading frame may have resulted from a
CC cloning artifact or may be due to misinterpretation of sequencing
CC data. This point has been overlooked on several occasions, with
CC the consequence of erroneous Alu-derived amino acid sequences
CC being reported.
CC -!- CAUTION: Any significant similarity of a putative protein sequence
CC with an Alu-translated entry must be taken as a warning that a
CC part of Alu repeat may have been artifactually included in the
CC coding nucleotide sequence.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U14571; -; NOT_ANNOTATED_CDS.
KW Hypothetical protein.
FT DOMAIN 1 95 Frame-1.
FT DOMAIN 99 193 Frame-2.
FT DOMAIN 197 291 Frame-3.
FT DOMAIN 295 389 Frame-4.
FT DOMAIN 393 487 Frame-5.
FT DOMAIN 491 585 Frame-6.
SQ SEQUENCE 585 AA; 63957 MW; 46EB8C4F493650A7 CRC64;
Query Match 17.8%; Score 73; DB 1; Length 585;
Best Local Similarity 80.0%; Pred. No. 1.8;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 SSSLGLPKCWDYRHE 15

Db 566 SARLGLPKCWDYRRE 580
|: ||||| |
RESULT 14
ALU2_HUMAN STANDARD; PRT; 587 AA.
ID ALU2_HUMAN
AC P39189;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alu subfamily SB sequence contamination warning entry.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95021758; PubMed=7935834; DOI=10.1038/371752a0;
RA Claverie J.-M., Makalowski W.;
RT "Alu alert.";
RL Nature 371:752-752(1994).
RN [2]
RP CONCEPT.
RX MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.;
RT "Identifying coding exons by similarity search: alu-derived and other
RT potentially misleading protein sequences.";
RL Genomics 12:838-841(1992).
RN [3]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA Quentin Y.;
RT "The Alu family developed through successive waves of fixation closely
RT connected with primate lineage history.";
RL J. Mol. Evol. 27:194-202(1988).
RN [4]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J., Milosavljevic A.;
RT "Reconstruction and analysis of human Alu genes.";
RL J. Mol. Evol. 32:105-121(1991).
CC -!- MISCELLANEOUS: Various analyses indicate that Alu repeats fall
CC into 8 subfamilies (Ref.3 and Ref.4). Therefore, 8 Alu warning
CC consensus sequences have been constituted that contain all six
CC frames conceptual translations of each of these classes of Alu
CC repeats.
CC -!- MISCELLANEOUS: Isolated 'X' indicates the presence of a stop
CC codon, 'XXX' is used to separate the various translation phases.
CC -!- CAUTION: This Alu entry is provided in order to avoid the further
CC pollution of protein sequence databases with Alu-derived amino
CC acid sequences.
CC -!- CAUTION: Alu repetitive sequences are interspersed in human and
CC primate genomes with an average spacing of 4 kb. Some of them are
CC actively transcribed by pol III. Normal transcripts may contain
CC Alu-derived sequences in 5' or 3' untranslated regions. However,
CC cDNA libraries also contain partial and/or rearranged cDNAs
CC ligated with Alu-derived sequence in any orientation. Although Alu
CC elements (especially situated on the complementary strand) have a
CC great potential to create additional/alternative exons,
CC consideration should be given to the possibility that the presence
CC of an Alu in an open reading frame may have resulted from a
CC cloning artifact or may be due to misinterpretation of sequencing
CC data. This point has been overlooked on several occasions, with
CC the consequence of erroneous Alu-derived amino acid sequences
CC being reported.
CC -!- CAUTION: Any significant similarity of a putative protein sequence
CC with an Alu-translated entry must be taken as a warning that a
CC part of Alu repeat may have been artifactually included in the
CC coding nucleotide sequence.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL; U14568; -; NOT_ANNOTATED_CDS.

CC KW Hypothetical protein_96 Frame-1.
 CC FT DOMAIN 1 96 Frame-2.
 CC FT DOMAIN 100 194 Frame-3.
 CC FT DOMAIN 198 292 Frame-4.
 CC FT DOMAIN 296 391 Frame-5.
 CC FT DOMAIN 395 489 Frame-6.
 CC FT DOMAIN 493 587
 CC SQ SEQUENCE 587 AA; 63703 MW; 3FAAB3E3E3929203 CRC64;

Query Match 17.8%; Score 73; DB 1; Length 587;
 Best Local Similarity 80.0%; Pred. No. 1.8;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SSSLGPKCWDYRHE 15
 Db 372 SARLGPKCWDYRRE 386
 | : |||||

RESULT 15

ALU3_HUMAN STANDARD; PRT; 587 AA.
 AC P39190;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alu subfamily SBI sequence contamination warning entry.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=92241891; PubMed=1572661;
 RA Claverie J.-M.;
 RT "Identifying coding exons by similarity search: alu-derived and other
 RT potentially misleading protein sequences.";
 RL Genomics 12:838-841(1992).
 [3]
 RN ALU FAMILIES CLASSIFICATION.
 RP MEDLINE=88333009; PubMed=3138422;
 RA Quentín Y.;
 RT "The Alu family developed through successive waves of fixation closely
 RT connected with primate lineage history.";
 RL J. Mol. Evol. 27:194-202(1988).
 [4]
 RN ALU FAMILIES CLASSIFICATION.
 RP MEDLINE=9117815; PubMed=1706781;
 RA Jurka J., Mišosavljević A.;
 RT "Reconstruction and analysis of human Alu genes.";
 RL J. Mol. Evol. 32:105-121(1991).
 CC -!- MISCELLANEOUS: Various analyses indicate that Alu repeats fall
 CC into 8 subfamilies (Ref.3 and Ref.4). Therefore, 8 Alu warning
 CC consensus sequences have been constituted that contain all six
 CC frames conceptual translations of each of these classes of Alu
 CC repeats.
 CC -!- MISCELLANEOUS: Isolated 'x' indicates the presence of a stop
 CC codon, 'xxx' is used to separate the various translation phases.
 CC -!- CAUTION: This Alu entry is provided in order to avoid the further
 CC pollution of protein sequence databases with Alu-derived amino
 CC acid sequences.

CC -!- CAUTION: Alu repetitive sequences are interspersed in human and
 CC primate genomes with an average spacing of 4 kb. Some of them are
 CC actively transcribed by pol III. Normal transcripts may contain
 CC Alu-derived sequences in 5' or 3' untranslated regions. However,
 CC cDNA libraries also contain partial and/or rearranged cDNAs
 CC ligated with Alu-derived sequence in any orientation. Although Alu
 CC elements (especially situated on the complementary strand) have a
 CC great potential to create additional/alternative exons,
 CC consideration should be given to the possibility that the presence
 CC of an Alu in an open reading frame may have resulted from a
 CC cloning artifact or may be due to misinterpretation of sequencing
 CC data. This point has been overlooked on several occasions, with
 CC the consequence of erroneous Alu-derived amino acid sequences
 CC being reported.
 CC -!- CAUTION: Any significant similarity of a putative protein sequence
 CC with an Alu-translated entry must be taken as a warning that a
 CC part of Alu repeat may have been artifactually included in the
 CC coding nucleotide sequence.

CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; U14569; -; NOT_ANNOTATED_CDS.
 CC KW Hypothetical protein.
 CC FT DOMAIN 1 96 Frame-1.
 CC FT DOMAIN 100 194 Frame-2.
 CC FT DOMAIN 198 292 Frame-3.
 CC FT DOMAIN 296 391 Frame-4.
 CC FT DOMAIN 395 489 Frame-5.
 CC FT DOMAIN 493 587 Frame-6.
 CC SQ SEQUENCE 587 AA; 63573 MW; 85C4155726DEF235 CRC64;

Qy 1 SSSLGPKCWDYRHE 15
 Db 372 SARLGPKCWDYRRE 386
 | : |||||

Search completed: October 11, 2005, 07:18:51
 Job time : 47.0201 secs

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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 55.5481 Seconds
(without alignments)
522.196 Million cell updates/sec

Title: US-10-092-934-7

Perfect score: 409

Sequence: 1 SSSLGIPKCDWRHLLSLA.....CPVKIALLTINGHCTWLPAS 75

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	409	100.0	75	2	AAR63238 Neural th
2	409	100.0	75	2	AAR95917 AD 16C-T7
3	409	100.0	75	5	AAE29148 Neural th
4	409	100.0	75	6	ABR63246 75 amino
5	409	100.0	75	6	ABU02978 Human neu
6	409	100.0	75	6	ABP59928 Human 75
7	409	100.0	75	6	AAE33195 Neural th
8	409	100.0	75	6	ABJ19451 75-mer ne
9	409	100.0	75	7	ADB37525 Neural th
10	409	100.0	75	7	ADL96026 Human neu
11	98	24.0	59	4	AAO02982 Human pol
12	98	24.0	109	4	AAO06037 Human pol
13	97	23.7	138	4	AAU31559 Novel hum
14	93	22.7	64	4	AAO03740 Human pol
15	92	22.5	62	4	AAO00751 Human pol
16	92	22.5	86	4	AAU22283 Human car
17	92	22.5	86	7	ADE46251 Human car
18	92	22.5	86	8	ADJ07669 Human car
19	91	22.2	74	4	AAAM86645 Human imm
20	91	22.2	77	4	AAO07835 Human pol
21	91	22.2	104	4	AAO04575 Human pol
22	90	22.0	15	6	ABP59914 Human neu
23	90	22.0	15	7	ADL96060 Human neu
24	90	22.0	37	4	AAO09372 Human pol
25	89.5	21.9	112	4	AAO04265 Human pol

26	89	21.8	15	6	ABP59911	Human neu
27	89	21.8	15	7	ADL96057	Human neu
28	89	21.8	47	3	AAAB25722	Human sec
29	89	21.8	202	8	ADRO9020	Human pro
30	88.5	21.6	47	4	AAU20869	Human nov
31	88	21.5	107	4	AAO04057	Human pol
32	87	21.3	44	4	AAAM82609	Human imm
33	87	21.3	45	4	AAO04635	Human pol
34	87	21.3	70	4	AAO02710	Human pol
35	86.5	21.1	104	4	ABG07702	Novel hum
36	86	21.0	72	2	AAAY02926	Fragment
37	86	21.0	72	7	ADA07757	Human sec
38	86	21.0	72	8	ADN41484	Novel hum
39	86	21.0	87	5	ADK34159	Novel hum
40	85.5	20.9	109	4	AAO02394	Human pol
41	85	20.8	15	6	ABP59915	Human neu
42	85	20.8	15	7	ADL96061	Human neu
43	85	20.8	58	4	AAO03818	Human pol
44	85	20.8	82	4	AAAG73475	Human gen
45	85	20.8	104	4	AAAM89847	Human imm

ALIGNMENTS

RESULT 1
AAR63238
ID AAR63238 standard; protein; 75 AA.
XX AC AAR63238;
XX AC AAR63238;
DT 25-MAR-2003 (revised)
DT 06-JUL-1995 (first entry)
XX XX
DE Neural thread protein AD16C T7.
XX KW Neural thread protein AD16C T7; Alzheimer's; neuroectodermal tumours;
KW KW malignant astrocytomas; glioblastomas.
XX OS Rattus rattus.
XX FH Key Location/Qualifiers
FT Misc-difference 1..75
FT FT /note= "corresponding codons 1..184, AAQ77882"
XX XX
PN WO9423756-A1.
XX XX
PD 27-OCT-1994.
XX XX
PF 20-APR-1994; 94WO-US004321.
XX XX
PR 20-APR-1993; 93US-00050559.
XX XX
PA (GEO) GEN HOSPITAL CORP.
XX XX
PI De La Monte SM, Wands JR;
XX XX
DR WPI; 1994-341497/42.
DR N-PSDB; AAQ77882.
XX XX
PS Detection of neural thread proteins - to detect sporadic and familial
PT Alzheimer's disease, neuroectodermal tumours, malignant astrocytomas and
PT glioblastomas (Eng).
XX XX
XX Example 4; Fig 160; 158pp; English.
XX AAQ77882 encodes AAR63237 the AD16C T7 neural thread protein (NTP). These
CC sequences were used in the development of an antibody dependent method,
CC for the detection of NTPs. This new method could be used to diagnose
CC Alzheimer's disease (differentiating between sporadic and familial),
CC neuroectodermal tumours, malignant astrocytomas and glioblastomas.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX XX

SQ		Sequence 75 AA;	
Query Match		100.0%; Score 409; DB 2; Length 75;	
Best Local Similarity		100.0%; Pred. No. 9e-44;	
Matches 75;		Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	SSSLGPKCWDYRHELLSLALMINFRVMAC	TFQHIELRQKISIVPRKLC
	60		
Db	1	SSSLGPKCWDYRHELLSLALMINFRVMAC	TFQHIELRQKISIVPRKLC
	60		
QY	61	ALLTINGHCTWLPAS	75
	61	ALLTINGHCTWLPAS	75
RESULT 2			
AAR95917			
ID AAR95917 standard; protein; 75 AA.			
AC AAR95917;			
DT 14-NOV-1996 (first entry)			
DE AD 16c-T7 human neural thread protein clone (partial sequence).			
KW Neural thread protein; NTP; diagnosis; detection; Alzheimer's disease;			
KW neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;			
KW binding fragment.			
OS Homo sapiens.			
PN WO9615272-A1.			
PD 23-MAY-1996.			
PF 14-NOV-1995; 95WO-US017111.			
PR 14-NOV-1994; 94US-00340426.			
PA (GEO) GEN HOSPITAL CORP.			
PI De La Monte S, Wands JR;			
XX WPI; 1996-259865/26.			
PT Detection of neural thread protein in diagnosis of Alzheimer's disease -			
PT also NTP DNA and protein sequences used in gene and anti-sense therapy.			
PS Example 4c; Fig 160; 238pp; English.			
CC A method for detecting the presence of neural thread protein (NTP) having			
CC a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject			
CC comprises (a) contacting a sample from a human subject that is suspected			
CC of containing the NTP with at least one molecule capable of binding to			
CC the protein; and (b) detecting any of the molecule bound to the protein.			
CC The binding molecule is selected from an antibody free of natural			
CC impurities, a monoclonal antibody or a binding fragment of either of			
CC these. The method may be used for diagnosing the presence of Alzheimer's			
CC disease, neuroectodermal tumours and a malignant astrocytoma in a human.			
CC A number of clones of neural thread protein were isolated from healthy 17			
CC -18 week old foetal human brain (HB) 2 year old temporal lobe neocortex			
CC and end stage Alzheimer's disease (AD) cerebral cortex. See AAT27753-75			
XX Sequence 75 AA;			
Query Match		100.0%; Score 409; DB 2; Length 75;	
Best Local Similarity		100.0%; Pred. No. 9e-44;	
Matches 75;		Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	SSSLGPKCWDYRHELLSLALMINFRVMAC	TFQHIELRQKISIVPRKLC
	60		
Db	1	SSSLGPKCWDYRHELLSLALMINFRVMAC	TFQHIELRQKISIVPRKLC
	60		

QY		61 ALLTINGHCTWLPAS 75	
Db		61 ALLTINGHCTWLPAS 75	
RESULT 3			
AAE29148			
ID AAE29148 standard; protein; 75 AA.			
AC AAE29148;			
DT 27-JAN-2003 (first entry)			
DE Neural thread protein (NTP) #6.			
KW Neural thread protein; NTP; hyperplasia; hypertrophy; arteriosclerosis;			
KW haemorrhoid; gene therapy; tumour; vascular disease; atherosclerosis;			
KW inflammatory disease; nutritional deficiency disease; genetic disease;			
KW autoimmune disease; metabolic disease; traumatic disease; intoxication;			
KW infectious disease; congenital malformation; enzyme deficiency disease;			
KW amyloid disease; fibrosis disease; storage disease; radiation disease;			
KW poisoning; environmental disease; endocrine disease; protein therapy;			
KW degenerative disease; mechanical disease.			
OS Unidentified.			
XX WO200274323-A2.			
PD 26-SEP-2002.			
PF 08-MAR-2002; 2002WO-IB001959.			
PR 08-MAR-2001; 2001US-0273957P.			
PA (AVER/) AVERBACK P.			
PI Avertack P;			
XX WPI; 2002-759864/82.			
PT Treating a condition in a patient requiring removal or destruction of			
PT cells, such as a benign or malignant tumor of a tissue or an inflammatory			
PT disease, comprises administering a neural thread protein (NTP) or a NTP			
PT gene to a mammal.			
XX Claim 23; Fig 7; 70pp; English.			
CC The invention relates to a method for treating a condition in a patient			
CC requiring removal or destruction of cells. The method involves			
CC administering to a mammal a neural thread protein (NTP), or administering			
CC to a tumour or other target cell a NTP gene, where the expression of the			
CC NTP gene is induced resulting in expression of the NTP protein. The			
CC method and NTP are useful for treating a condition in a patient requiring			
CC removal or destruction of cells, such as a benign or malignant tumour of			
CC a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue,			
CC preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,			
CC bacterially, or parasitically altered tissue, or a malformation of a			
CC tissue. Other conditions include a cosmetic modification to a tissue,			
CC such as removal of unwanted facial hair, warts or unwanted fatty tissue,			
CC a vascular disease, particularly atherosclerosis or arteriosclerosis,			
CC haemorrhoids, or varicose veins, an inflammatory disease, autoimmune			
CC disease, metabolic disease, hereditary/genetic disease, traumatic disease			
CC or physical injury, nutritional deficiency disease, infectious disease,			
CC congenital malformation, amyloid disease, fibrosis disease, storage			
CC disease, enzyme deficiency disease, poisoning, intoxication, degenerative			
CC disease, radiation disease, environmental disease, endocrine disease or			
CC mechanical disease. The invention is useful in protein therapy and gene			
CC therapy. The present sequence is NTP protein			
XX Sequence 75 AA;			
Query Match		100.0%; Score 409; DB 5; Length 75;	
Best Local Similarity		100.0%; Pred. No. 9e-44;	

Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSGLPKCWDYRHELLSLALMINFRVWACTFKQHIELRQKISIVPRKLCMGVPCVKI 60
Db 1 SSSGLPKCWDYRHELLSLALMINFRVWACTFKQHIELRQKISIVPRKLCMGVPCVKI 60
QY 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 4
ABR63246
ID ABR63246 standard; protein; 75 AA.
XX ABR63246;
AC
XX
DT 28-AUG-2003 (first entry)
XX
DE 75 amino acid neural thread protein.
XX
KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour.
XX
OS Unidentified.
XX
PN WO2003008443-A2.
XX
XX 30-JAN-2003.
XX
XX 19-JUL-2002; 2002WO-CA001105.
XX
PR 19-JUL-2001; 2001US-0306150P.
PR 19-JUL-2001; 2001US-0306161P.
PR 16-NOV-2001; 2001US-0331477P.
XX
XX (NYMO-) NYMOX CORP.
PA
XX
PI Averbach PA;
XX
XX WPI; 2003-247999/24.
XX
PT Novel neural thread protein peptide, referred as cell death peptide,
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
XX
PS Disclosure; Fig 7; 77pp; English.
XX
XX The present invention relates to a neural thread protein (NTP) peptide
XX referred to as cell death peptide. Thought to be cytostatic,
XX antibacterial, immunosuppressive and antiinflammatory. It is useful for
XX treating a condition in a patient requiring removal or destruction of
XX cells, for treating a condition such as benign or malignant tumor.
XX inflammatory disease, autoimmune disease and infectious disease. The
XX peptide useful for treatment is derived from the amino acid sequence for
XX a pancreatic thread protein. The peptide is conjugated, linked or bound
XX to a molecule chosen from antibody or its fragment, antibody-like binding
XX molecule, where the molecule has a higher affinity for binding to a tumor
XX or other target than binding to other cells. Treatment using NTP peptides
XX can remove benign tumors with less risk and fewer of the undesirable side
XX effects of surgery. The present sequence is an NTP amino acid sequence
XX
SQ Sequence 75 AA;

Query Match 100.0%; Score 409; DB 6; Length 75;
Best Local Similarity 100.0%; Pred. No. 9e-44;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSGLPKCWDYRHELLSLALMINFRVWACTFKQHIELRQKISIVPRKLCMGVPCVKI 60
Db 1 SSSGLPKCWDYRHELLSLALMINFRVWACTFKQHIELRQKISIVPRKLCMGVPCVKI 60
QY 61 ALLTINGHCTWLPAS 75

Db 61 ALLTINGHCTWLPAS 75

RESULT 5
ABU02978
ID ABU02978 standard; protein; 75 AA.
XX
XX ABU02978;
AC
XX
DT 20-JAN-2003 (first entry)
XX
DE Human neural thread protein AD7C-NTP, protein fragment #6.
XX
KW Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;
KW transplantation; grafting; chemotherapy; immunotherapy; vaccination;
KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;
KW radiation; tumour; hyperplasia; hypertrophy; overgrowth of tissue;
KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;
KW cosmetic modification; vascular disease; atherosclerosis;
KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;
KW autoimmune disease; metabolic disease; traumatic disease;
KW physical injury; nutritional deficiency disease; infectious disease;
KW amyloid disease; fibrosis disease; storage disease;
KW congenital malformation; enzyme deficiency disease; poisoning;
KW intoxication; environmental disease; radiation disease;
KW endocrine disease; degenerative disease; mechanical disease.
XX
OS Homo sapiens.
XX
XX WO200297030-A2.
XX
XX 05-DEC-2002.
XX
XX 24-MAY-2002; 2002WO-CA000759.
XX
XX 25-MAY-2001; 2001US-0293156P.
XX
XX (NYMO-) NYMOX CORP.
PA
XX
PI Averbach PA;
XX
XX WPI; 2003-041406/03.
XX
XX Novel peptides similar in amino acid sequence to neural thread proteins
XX (NTP), useful for treating unwanted cellular proliferations such as
XX malignant tumors and prostatic hyperplasia.
XX
XX Disclosure; Fig 7; 78pp; English.
XX
XX The invention describes an NTP-peptide (I) comprising at least one amino
XX acid sequence corresponding to part of the amino acid sequence of a
XX neural thread protein, AD7C-NTP. The invention provides a method of
XX treating a condition requiring removal or destruction of cells of a
XX mammal comprising administering to a mammal, a therapeutic amount of (I).
XX The treatment is administered to the mammal before, during or after
XX surgical excision, transplantation, grafting, chemotherapy,
XX immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,
XX laser therapy, phototherapy, gene therapy and/or radiation. The method is
XX useful for treatment of benign or malignant tumour; hyperplasia,
XX hypertrophy or overgrowth of tissue; virally, bacterially or
XX parasitically altered tissue; malformation of tissue selected from lung,
XX breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,
XX sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary
XX gland, blood, brain and its coverings, spinal cord, muscle, connective
XX tissue, adrenal, parathyroid thyroid, uterus, testis, pituitary,
XX reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,
XX tonsils, mouth and lymph nodes and lymphoid system; tonsillary
XX hypertrophy; prostatic hyperplasia; cosmetic modification to a tissue;
XX vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;
XX varicose veins; inflammatory disease; autoimmune disease; metabolic
XX disease; hereditary/genetic disease; traumatic disease; physical injury;
XX nutritional deficiency disease; infectious disease; amyloid disease;

CC fibrosis disease; storage disease; congenital malformation; enzyme
CC deficiency disease; poisoning; intoxication; environmental disease;
CC radiation disease; endocrine disease; degenerative disease and mechanical
CC disease. This is the amino acid sequence of a human neural thread protein
CC AD7C-NTP protein fragment
XX
SQ Sequence 75 AA;

Query Match 100.0%; Score 409; DB 6; Length 75;
Best Local Similarity 100.0%; Pred. No. 9e-44;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSLGLPKCWDYRHELLSLALMINFRVMACCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
Db 1 SSSLGLPKCWDYRHELLSLALMINFRVMACCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60

QY 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 6
ABP59928
ID ABP59928 standard; protein; 75 AA.
XX
AC ABP59928;
XX
DT 08-SEP-2003 (first entry)
XX
DE Human 75 amino acid neural thread protein.
XX
KW Human; tumour; cancer; neural thread protein; NTP; cell removal;
KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;
KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003044053-A2.
XX
PD 30-MAY-2003.
XX
PF 18-NOV-2002; 2002WO-CA001757.
XX
PR 16-NOV-2001; 2001US-0331477P.
XX
PA (NYMO-) NYMOX CORP.
XX
PI Averbach P, Gemmell J;
XX
DR WPI; 2003-457592/43.
XX
PT New neural thread protein (NTP); useful for preparing a composition for
PT treating or preventing a condition in a mammal requiring removal or
PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or
PT inflammatory disease.
XX
PS Disclosure; Fig 5; 98pp; English.
XX
CC The present invention relates to peptides derived from the human neural
CC thread protein (NTP). The peptides are useful for preparing a composition
CC for treating or preventing a condition in a mammal requiring removal or
CC destruction of cells, comprising tonsillary hypertrophy, prostatic
CC hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a
CC breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,
CC varicose veins, atherosclerosis, inflammatory, metabolic, infectious,
CC fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,
CC occlusion or blockage of an artery or of a stent placed or implanted in
CC an artery. The present sequence is an NTP protein used to produce
CC peptides of the invention
XX
SQ Sequence 75 AA;

Query Match 100.0%; Score 409; DB 6; Length 75;
Best Local Similarity 100.0%; Pred. No. 9e-44;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSLGLPKCWDYRHELLSLALMINFRVMACCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
Db 1 SSSLGLPKCWDYRHELLSLALMINFRVMACCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60

QY 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 7
AAE33195
ID AAE33195 standard; protein; 75 AA.
XX
AC AAE33195;
XX
DT 16-APR-2003 (first entry)
XX
DE Neural thread protein (NTP) #6.
XX
KW Cell death; tissue necrosis; neural thread protein; NTP; amyloidosis;
KW stroke; brain tumour; Pick's disease; Parkinson's disease; glaucoma;
KW Alzheimer's disease; gene therapy.
XX
OS Unidentified.
XX
PN WO200289841-A2.
XX
PD 14-NOV-2002.
XX
PF 06-MAY-2002; 2002WO-CA000681.
XX
PR 04-MAY-2001; 2001US-0288463P.
XX
PA (NYMO-) NYMOX CORP.
XX
PI Averbach PA;
XX
DR WPI; 2003-120506/11.
XX
PT Preventing, controlling, modulating, ameliorating and/or treating cell
PT death or tissue necrosis using antibodies to neural thread proteins
PT useful in disorders such as stroke, brain tumor, glaucoma and Alzheimer's
PT disease.
XX
PS Disclosure; Fig 10; 60pp; English.
XX
CC The invention relates to a method of preventing, and/or inhibiting cell
CC death and/or tissue necrosis in live tissue containing neural thread
CC proteins (NTP). The method involves contacting the live tissue with at
CC least one antibody, fragment or derivative that recognises NTP, where the
CC antibody, fragment or derivative is present to prevent, control,
CC ameliorate and/or inhibit cell death and/or tissue necrosis caused by the
CC presence of NTP. Methods and compositions of the invention are useful for
CC preventing, modulating, controlling and/or treating disorders associated
CC with cell death and/or tissue necrosis such as stroke, brain tumour,
CC Pick's disease, Parkinson's disease, amyloidosis, glaucoma and
CC Alzheimer's disease. The invention is useful in gene therapy. The present
CC sequence is NTP protein
XX
SQ Sequence 75 AA;

Query Match 100.0%; Score 409; DB 6; Length 75;
Best Local Similarity 100.0%; Pred. No. 9e-44;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSLGLPKCWDYRHELLSLALMINFRVMACCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
Db 1 SSSLGLPKCWDYRHELLSLALMINFRVMACCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60

QY 61 ALLTINGHCTWLPAS 75
 Db 61 ALLTINGHCTWLPAS 75

RESULT 8
 ABJ19451
 ID ABJ19451 standard; protein; 75 AA.
 AC ABJ19451;
 DT 27-MAR-2003 (first entry)
 XX
 XX 75-mer neural thread protein.
 DE
 XX Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
 KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.
 KW
 OS Unidentified.
 XX
 XX WO200292115-A2.
 PN
 XX 21-NOV-2002.
 XX
 XX 16-MAY-2002; 2002WO-CA000712.
 PF
 XX 16-MAY-2001; 2001US-0290971P.
 PR
 XX (NYMO-) NYMOX CORP.
 PA
 XX Averbach PA;
 PI
 XX WPI; 2003-129234/12.
 DR
 XX Preventing and/or inhibiting cell death and/or tissue necrosis in a
 PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
 PT disease, by contacting the live tissue with at least one segment of
 PT neural thread proteins (NTP).
 XX
 XX Disclosure; Fig 7; 60pp; English.

XX The invention relates to a novel method for preventing and/or inhibiting
 CC cell death and/or tissue necrosis in a tissue comprising contacting the
 CC live tissue with at least one segment of neural thread proteins (NTP).
 CC The methods are composition are useful for treating a neurodegenerative
 CC disorder, such as Alzheimer's disease. This sequence represents an NTP
 CC protein of the invention
 CC
 XX Sequence 75 AA;
 SQ
 Query Match 100.0%; Score 409; DB 6; Length 75;
 Best Local Similarity 100.0%; Pred. No. 9e-44;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSGLPKCWDYRHEHLSLALMINFRVWACTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
 Db 1 SSSGLPKCWDYRHEHLSLALMINFRVWACTFKQHIELRQKISIVPRKLCMGPVCPVKI 60

QY 61 ALLTINGHCTWLPAS 75
 Db 61 ALLTINGHCTWLPAS 75

RESULT 9
 ADB37525
 ID ADB37525 standard; protein; 75 AA.
 AC ADB37525;
 XX
 XX 04-DEC-2003 (first entry)
 DT
 XX Neural thread protein #4.
 DE
 XX

KW Cytostatic; Antitumour; Antipsoxiatic; Dermatological;
 KW Antiatherosclerotic; Antiarteriosclerotic; Vasotropic; Antiinflammatory;
 KW Immunosuppressive; Tranquillizer; Antileptic; Virucide; AD7c-NTP;
 KW neural thread protein; neuritic sprouting.
 XX
 OS Unidentified.
 XX
 XX WO2003008444-A2.
 PN
 XX 30-JAN-2003.
 PD
 XX
 XX 19-JUL-2002; 2002WO-CA001106.
 PF
 XX 19-JUL-2001; 2001US-0306150P.
 PR
 XX 19-JUL-2001; 2001US-0306161P.
 PR
 XX 16-NOV-2001; 2001US-0331477P.
 XX
 XX (NYMO-) NYMOX CORP.
 PA
 XX Averbach PA, Gemmell J;
 PI
 XX WPI; 2003-248000/24.
 DR
 XX
 XX Novel Related peptide or AD7c-neural thread peptide, useful for treating
 PT unwanted cellular proliferations, glandular hyperplasia, unwanted facial
 PT hair, warts and unwanted fatty tissue.
 XX
 XX Disclosure; Fig 7; 109pp; English.

XX The present invention relates to AD7c-neural thread protein (NTP) and
 CC related proteins and peptides (I; ADB37528-ADB37641). The sequences are
 CC useful for treating a condition in a patient requiring removal or
 CC destruction of cells. The condition can be selected from benign or
 CC malignant tumour of a tissue, hyperplasia, hypertrophy or overgrowth of a
 CC tissue, virally, bacterially or parasitically altered tissue, or
 CC malformation of a tissue, where the tissue is selected from lung, breast,
 CC stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney, sinus,
 CC colon, intestine, stomach, rectum, oesophagus, heart, spleen, salivary
 CC gland, blood, brain and its coverings, spinal cord and its coverings,
 CC muscle, connective tissue, adrenal, parathyroid, thyroid, uterus, testis,
 CC pituitary, reproductive organs, liver, gall bladder, eye, ear, nose,
 CC throat, tonsils, mouth, lymph nodes and lymphoid tissue. The condition is
 CC preferably tonsillary hypertrophy, prostatic hyperplasia, psoriasis,
 CC eczema, dermatosis, cosmetic modification to a tissue (skin, eye, ear,
 CC nose, throat, mouth, muscle, connective, hair or breast tissue), vascular
 CC disease (atherosclerosis or arteriosclerosis), haemorrhoids, varicose
 CC veins, inflammatory disease, autoimmune disease, metabolic disease,
 CC hereditary/genetic disease, traumatic disease or physical injury,
 CC nutritional deficiency disease, infectious disease, amyloid disease,
 CC fibrosis disease, storage disease, congenital malformation, enzyme
 CC deficiency disease, poisoning, intoxication, environmental disease,
 CC radiation disease, endocrine disease, degenerative disease and mechanical
 CC disease. The peptides are useful for treating unwanted cellular
 CC proliferations, glandular (e.g. prostate) hyperplasia, unwanted facial
 CC hair, warts and unwanted fatty tissue, or for preparing antibodies that
 CC recognize and/or bind to Related proteins, Related peptides or NTP
 CC peptides. The present sequence was used to illustrate the invention.
 XX
 XX Sequence 75 AA;
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 Query Match 100.0%; Score 409; DB 7; Length 75;
 Best Local Similarity 100.0%; Pred. No. 9e-44;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSGLPKCWDYRHEHLSLALMINFRVWACTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
 Db 1 SSSGLPKCWDYRHEHLSLALMINFRVWACTFKQHIELRQKISIVPRKLCMGPVCPVKI 60

QY 61 ALLTINGHCTWLPAS 75
 Db 61 ALLTINGHCTWLPAS 75

RESULT 10	
ADL96026	ADL96026 standard; protein; 75 AA.
ID	
XX	
AC	ADL96026;
XX	
DT	20-MAY-2004 (first entry)
XX	
XX	Human neural thread protein, NTP75.
XX	
KW	Human; neural thread protein; NTP122; NTP112; NTP106; NTP98; NTP75;
KW	NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;
KW	eczema; haemorrhoid; atherosclerosis; inflammatory disease;
KW	autoimmune disease; metabolic disease; hereditary disease;
KW	genetic disease; traumatic disease; infectious disease; amyloid disease;
KW	nutritional deficiency disease; storage disease; congenital malformation;
KW	Alzheimer's disease; storage disease; poisoning; intoxication;
KW	enzyme deficiency disease; radiation disease; endocrine disease;
KW	degenerative disease; mechanical disease.
XX	
OS	Homo sapiens.
XX	
PN	US2003166569-A1.
XX	
PD	04-SEP-2003.
XX	
PF	15-NOV-2002; 2002US-00294891.
XX	
PR	16-NOV-2001; 2001US-0331477P.
XX	
PA	(AVER/) AVERBACK P.
PA	(GEMM/) GEMMELL J.
XX	
PI	Averback P, Gemmell J;
XX	
DR	WPI; 2003-898099/82.
XX	
PT	New neural thread protein or its variants, useful for treating tumors and
PT	other conditions requiring the removal or destruction of cells (e.g.
PT	prostatic hyperplasia, psoriasis, eczema, hemorrhoids or
PT	atherosclerosis).
XX	
PS	Disclosure; SEQ ID NO 5; 32pp; English.
XX	
CC	The invention relates to a peptide, or its homologue, derivative,
CC	fragment, variant or mimetic, comprising at least one neural thread
CC	protein (NTP) peptide appearing as ADL96029-ADL96069, derived from
CC	NTP132, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid
CC	encoding an amino acid sequence corresponding to the above peptide, a
CC	composition comprising one or more peptides or nucleic acids cited above
CC	and a carrier, a method of treating a condition in a mammal requiring
CC	removal or destruction of cells (comprising administering to the mammal
CC	an amount of the peptide cited above) and a method of preventing or
CC	inhibiting the stenosis, occlusion or blockage of a stent, comprising
CC	coating the stent with an amount of the above peptide. The peptide
CC	further comprises an amino acid in a reverse-D order based on the above
CC	amino acid sequences. The composition and methods are useful in treating
CC	tumours and other conditions requiring the removal or destruction of
CC	cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or
CC	atherosclerosis). These may also be used in treating inflammatory
CC	diseases, autoimmune diseases, metabolic diseases, hereditary/genetic
CC	diseases, traumatic diseases or physical injuries, nutritional deficiency
CC	diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,
CC	storage diseases, congenital malformation, enzyme deficiency disease,
CC	poisoning, intoxication, environmental diseases, radiation diseases,
CC	endocrine diseases, degenerative diseases or mechanical diseases. The
CC	present sequence is a human NTP protein from which the peptides of the
CC	invention are derived.
XX	
SQ	Sequence 75 AA;

Query Match 100.0%; Score 409; DB 7; Length 75;

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Best Local Similarity 100.0%; Pred.No.9e-44;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 SSSLGLPKCDWYRHELLSLALMINFRVMACTFKQHIELROKISIVPRKLCCMGPVCPVKI 60

Qy 61 ALLTINGHCTWLSPAS 75
Db | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 ALLTINGHCTWLSPAS 75

RESULT 11
AAO02982
ID ID AAO02982 standard; protein; 59 AA.
XX
AC AAO02982;
XX
DT DT 06-NOV-2001 (first entry)
XX
DE DE Human polypeptide SEQ ID NO 16874.
XX
KW KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW KW nervous system disorders; arthritis; inflammation.
XX
OS OS Homo sapiens.
XX
PN PN WO200164835-A2.
XX
PD PD 07-SEP-2001.
XX
PF PF 26-FEB-2001; 2001WO-US004927.
XX
PR PR 28-FEB-2000; 2000US-00515126.
PR PR 18-MAY-2000; 2000US-00577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI PI Tang YT, Liu C, Drmanac RT;
XX
DR DR WPI; 2001-514838/56.
XX
DR DR N-PSDB; AAI82913.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT PT and treating e.g. leukemia, inflammation and immune disorders.
XX
PS PS Claim 20; SEQ ID NO 16874; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC CC the encoded proteins (AAO0010-AAO13910) that exhibit activity relating to
CC CC cytokine, cell proliferation or cell differentiation or which may induce
CC CC production of other cytokines in other cell populations. The
CC CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC CC peptide therapy. The polypeptides have various cytokine-like activities,
CC CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC CC activity, tissue growth factor activity, immunomodulatory activity and
CC CC activin/inhibin activity and may be useful in the diagnosis and/or
CC CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC CC inflammation. Note: The sequence data for this patent did not form part
CC CC of the printed specification, but was obtained in electronic format
CC CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 59 AA;

Query Match 24.0%; Score 98; DB 4; Length 59;
Best Local Similarity 51.1%; Pred.No.0.00014;
Matches 24; Conservative 3; Mismatches 8; Indels 12; Gaps 3;

Qy 1 SSSLGLPKCDWYRHELLSLALMI-----NFRVM---ACTFKQHIE 37
Db | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|
13 SACLGLPKCDWYRRPELPCALVILLTAKTNFIRVRKNVCVF--HVE 57

```

```

DE Novel human secreted protein #2050.
XX
XX Human; vaccination; gene therapy; nutritional supplement;
XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200179449-A2.
XX
XX 25-OCT-2001.
XX
XX 16-APR-2001; 2001WO-US008656.
XX
XX 18-APR-2000; 2000US-00552929.
XX
XX 26-JAN-2001; 2001US-00770160.
XX
XX (HYSE-) HYSEQ INC.
XX
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-611725/70.
XX
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
PT
XX
XX Claim 20; Page 458; 765pp; English.
XX
XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Calls
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU3304 represent the amino acid sequences of novel human
CC secreted proteins of the invention
XX
XX Sequence 138 AA;
SQ
Query Match 23.7%; Score 97; DB 4; Length 138;
Best Local Similarity 43.1%; Pred. No. 0.00049;
Matches 25; Conservative 6; Mismatches 23; Indels 4; Gaps 2
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AAO03740
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XX
XX AAO03740;
XX
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 17632.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW KW nervous system disorders; arthritis; inflammation.
XX
XX Homo sapiens.
OS

```


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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:16 ; Search time 125.735 Seconds
(without alignments)
248.149 Million cell updates/sec

Title: US-10-092-934-7
Perfect score: 409
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Scoring table: BLOSUM62
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Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	409	100.0	75	14 US-10-138-516-6	Sequence 6, Appli
2	409	100.0	75	14 US-10-146-130-8	Sequence 8, Appli
3	409	100.0	75	14 US-10-092-934-7	Sequence 7, Appli
4	409	100.0	75	14 US-10-153-334-7	Sequence 7, Appli
5	409	100.0	75	14 US-10-198-069-7	Sequence 7, Appli
6	409	100.0	75	14 US-10-198-070-7	Sequence 7, Appli
7	409	100.0	75	14 US-10-294-891-5	Sequence 5, Appli
8	409	100.0	75	17 US-10-920-313-5	Sequence 5, Appli
9	92	22.5	86	9 US-09-764-869-1057	Sequence 1057, Ap
10	92	22.5	86	14 US-10-091-504-1057	Sequence 1057, Ap
11	92	22.5	86	15 US-10-227-577-1057	Sequence 1057, Ap

12	90	22.0	15	14 US-10-294-891-39	Sequence 39, Appl
13	90	22.0	15	17 US-10-920-313-39	Sequence 39, Appl
14	89	21.8	15	14 US-10-294-891-36	Sequence 36, Appl
15	89	21.8	15	17 US-10-920-313-36	Sequence 36, Appl
16	89	21.8	47	11 US-09-985-153-111	Sequence 111, App
17	86.5	21.1	104	18 US-10-450-763-38061	Sequence 38061, A
18	86	21.0	72	10 US-09-983-802-578	Sequence 578, App
19	86	21.0	72	10 US-09-984-490-578	Sequence 578, App
20	86	21.0	72	11 US-09-973-278-606	Sequence 606, App
21	85	20.8	15	14 US-10-294-891-40	Sequence 40, Appl
22	85	20.8	15	17 US-10-920-313-40	Sequence 40, Appl
23	84.5	20.7	214	18 US-10-450-763-38139	Sequence 38139, A
24	84	20.5	70	9 US-09-764-877-2048	Sequence 2048, Ap
25	84	20.5	70	15 US-10-242-515-2048	Sequence 2048, Ap
26	83	20.3	43	9 US-09-764-860-344	Sequence 344, App
27	83	20.3	43	14 US-10-074-095-344	Sequence 344, App
28	83	20.3	43	15 US-10-212-872-344	Sequence 344, App
29	81	19.8	34	14 US-10-106-698-4417	Sequence 4417, Ap
30	81	19.8	102	15 US-10-104-047-3864	Sequence 3864, Ap
31	81	19.8	119	10 US-09-892-877-400	Sequence 400, App
32	81	19.8	119	10 US-09-948-783-400	Sequence 400, App
33	80	19.6	154	18 US-10-450-763-54264	Sequence 54264, A
34	77.5	18.9	72	18 US-10-820-474A-69	Sequence 69, Appl
35	77	18.8	241	15 US-10-276-774-1834	Sequence 1834, Ap
36	76	18.6	35	16 US-10-332-765-47	Sequence 47, Appl
37	76	18.6	152	15 US-10-104-047-2372	Sequence 2372, Ap
38	75	18.3	101	9 US-09-764-853-432	Sequence 432, App
39	75	18.3	119	9 US-09-764-847-696	Sequence 696, App
40	75	18.3	119	14 US-10-092-154-696	Sequence 696, App
41	75	18.3	121	9 US-09-764-877-1641	Sequence 1641, Ap
42	75	18.3	121	15 US-10-242-515-1641	Sequence 1641, Ap
43	75	18.3	127	11 US-09-833-245-1427	Sequence 1427, Ap
44	74	18.1	310	9 US-09-864-921-12	Sequence 12, Appl
45	74	18.1	310	17 US-10-766-682-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-10-138-516-6
; Sequence 6, Application US/10138516
; Publication No. US20030003445A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING ANTIBODIES TO
; TITLE OF INVENTION: NEURAL THREAD PROTEINS
; FILE REFERENCE: 59003.000004
; CURRENT APPLICATION NUMBER: US/10/138.516
; CURRENT FILING DATE: 2002-07-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-516-6

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Best Local Similarity 100.0%; Pred. No. 3.6e-43;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 8, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE OF INVENTION: NEURAL THREAD PROTEINS
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-8

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Best Local Similarity 100.0%; Pred. No. 3.6e-43;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSGLPKCWDYRHELLSLALMINFRVMACCTFKQHIELROKISIVPRKLCMGPVCPVKI 60
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Db 61 ALLTINGHCTWLPAS 75

RESULT 3
US-10-092-934-7
; Sequence 7, Application US/10092934
; Publication No. US20030054990A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHODS OF USING NEURAL THREAD PROTEINS TO TREAT TUMORS
; TITLE OF INVENTION: AND CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; FILE OF INVENTION: CELLS
; FILE REFERENCE: 018792-0199
; CURRENT APPLICATION NUMBER: US/10/092,934
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/273,957
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Neural thread
US-10-092-934-7

Query Match      100.0%; Score 409; DB 14; Length 75;
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Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 4
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; Sequence 7, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; FILE OF INVENTION: CELLS
; FILE REFERENCE: 59003-000006
; CURRENT APPLICATION NUMBER: US/10/153,334
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,156
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-334-7

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Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 5
US-10-198-069-7
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; Publication No. US20030096756A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; FILE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000009
; CURRENT APPLICATION NUMBER: US/10/198,069
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
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; SEQ ID NO 7
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown NTP
US-10-198-069-7

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Best Local Similarity 100.0%; Pred. No. 3.6e-43;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSGLPKCWDYRHELLSLALMINFRVMACCTFKQHIELROKISIVPRKLCMGPVCPVKI 60
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QY 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 6
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; Sequence 7, Application US/10198069
; Publication No. US20030096756A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; FILE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000009
; CURRENT APPLICATION NUMBER: US/10/198,069
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown NTP
US-10-198-069-7

Query Match      100.0%; Score 409; DB 14; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.6e-43;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSGLPKCWDYRHELLSLALMINFRVMACCTFKQHIELROKISIVPRKLCMGPVCPVKI 60
Db 1 SSSGLPKCWDYRHELLSLALMINFRVMACCTFKQHIELROKISIVPRKLCMGPVCPVKI 60

QY 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75
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US-10-198-070-7
; Sequence 7, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.00008
; CURRENT APPLICATION NUMBER: US/10/198.070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 7
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Unknown NTP
; OTHER INFORMATION: peptide
US-10-198-070-7

Query Match      100.0%; Score 409; DB 14; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.6e-43;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSGLPKCDYRHELLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
Db 1 SSSGLPKCDYRHELLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60

Qy 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 7
US-10-294-891-5
; Sequence 5, Application US/10294891
; Publication No. US2003016569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294.891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-5

Query Match      100.0%; Score 409; DB 14; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.6e-43;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSGLPKCDYRHELLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
Db 1 SSSGLPKCDYRHELLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60

Qy 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

US-10-198-070-7
; Sequence 7, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.00008
; CURRENT APPLICATION NUMBER: US/10/198.070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 7
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Unknown NTP
; OTHER INFORMATION: peptide
US-10-198-070-7

Query Match      100.0%; Score 409; DB 14; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.6e-43;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSGLPKCDYRHELLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
Db 1 SSSGLPKCDYRHELLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60

Qy 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 7
US-10-294-891-5
; Sequence 5, Application US/10294891
; Publication No. US2003016569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294.891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-5

Query Match      100.0%; Score 409; DB 14; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.6e-43;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSGLPKCDYRHELLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
Db 1 SSSGLPKCDYRHELLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60

Qy 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

US-10-920-313-5
; Sequence 5, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920.313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-5

Query Match      100.0%; Score 409; DB 17; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.6e-43;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSGLPKCDYRHELLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
Db 1 SSSGLPKCDYRHELLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60

Qy 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 8
US-10-920-313-5
; Sequence 5, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920.313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-5

Query Match      100.0%; Score 409; DB 17; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.6e-43;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSGLPKCDYRHELLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
Db 1 SSSGLPKCDYRHELLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60

Qy 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 9
US-09-764-869-1057
; Sequence 1057, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN ET AL.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764.869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1057
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (71)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (82)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-869-1057

Query Match      22.5%; Score 92; DB 9; Length 86;
Best Local Similarity 56.2%; Pred. No. 0.0015;
Matches 18; Conservative 3; Mismatches 7; Indels 4; Gaps 1;

Qy 1 SSSGLPKCDYRHELLSLALMINFRVMCTFK 32
Db 7 SSSGLPKCDYRHEPLYMAYIF----LRCTF 34
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RESULT 10
US-10-091-504-1057
; Sequence 1057, Application US/10091504
; Publication No. US2003005908A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007C1
; CURRENT APPLICATION NUMBER: US/10/091,504
; NUMBER OF SEQ ID NOS: 2442
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1057
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (71)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: misc_feature
; LOCATION: (82)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-091-504-1057

Query Match      22.5%; Score 92; DB 14; Length 86;
Best Local Similarity 56.2%; Pred. No. 0.0015;
Matches 18; Conservative 3; Mismatches 7; Indels 4; Gaps 1;

Qy 1 SSSGLPKCWDYRHELLSLALMIFRVMCTF 32
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Db 7 SSCLSLPKCWDYRHEPLYMAYIF----LRCTF 34

RESULT 11
US-10-227-577-1057
; Sequence 1057, Application US/10227577
; Publication No. US2004005575A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007C2
; CURRENT APPLICATION NUMBER: US/10/227,577
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/091,504
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2001-01-17
; PRIOR FILING DATE: 2001-01-17
; PRIOR FILING DATE: 2000-01-31
; PRIOR FILING DATE: 2000-02-04
; PRIOR FILING DATE: 2000-06-28
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-08-14
; PRIOR FILING DATE: 2000-08-14
; PRIOR FILING DATE: 2000-07-26
; PRIOR FILING DATE: 2000-07-26
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-08-14
; PRIOR FILING DATE: 2000-08-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1057
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens

Qy 1 SSSGLPKCWDYRHELLSLALMIFRVMCTF 32
   ||| ||||| ||||| ||| : |||
Db 7 SSCLSLPKCWDYRHEPLYMAYIF----LRCTF 34

RESULT 12
US-10-294-891-39
; Sequence 39, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-39

Query Match      22.0%; Score 90; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 PRKLCCMGVPCVKI 60
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Db 1 PRKLCCMGVPCVKI 15

RESULT 13
US-10-920-313-39
; Sequence 39, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-39

Query Match      22.0%; Score 90; DB 17; Length 15;
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Best Local Similarity 100.0%; Pred. No. 0.00042; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

Qy 46 PRKLCMGPCVPVKI 60
| | | | | | | | | | | | | | | |
Db 1 PRKLCMGPCVPVKI 15

RESULT 14

US-10-294-891-36
; Sequence 36, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-36

Query Match 21.8%; Score 89; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSLGLPKCWDYRHE 15
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Db 1 SSSLGLPKCWDYRHE 15

RESULT 15

US-10-920-313-36
; Sequence 36, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-36

Query Match 21.8%; Score 89; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSLGLPKCWDYRHE 15
| | | | | | | | | | | | | | | |
Db 1 SSSLGLPKCWDYRHE 15

Search completed: October 11, 2005, 07:39:46
Job time : 126.735 secs

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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:19 ; Search time 17.1457 Seconds
(without alignments)
326.535 Million cell updates/sec

Title: US-10-092-934-7

Perfect score: 409

Sequence: 1 SSSLGPKCWDYRHELLSLA.....CPVKIALLTINGHCTWLPAS 75

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Issued Patents AA:*
- 2: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 7: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	409	100.0	75	2	US-08-340-426D-48
3	409	100.0	75	2	US-08-450-673C-48
4	409	100.0	75	5	PCT-US95-17111A-48
5	86	21.0	72	3	US-09-227-357-578
6	81.5	19.9	55	4	US-09-513-999C-7795
7	75.5	18.5	82	4	US-09-513-999C-5298
8	73	17.8	135	4	US-09-685-166A-884
9	73	17.8	135	4	US-09-679-426-884
10	73	17.8	135	4	US-09-759-143-884
11	72	17.6	24	4	US-09-461-325-436
12	72	17.6	24	4	US-10-012-542-436
13	72	17.6	24	4	US-10-115-123-436
14	71.5	17.5	397	5	PCT-US95-17111A-121
15	70	17.1	132	4	US-09-636-215-573
16	70	17.1	132	4	US-09-685-166A-573
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18	70	17.1	132	4	US-09-759-143-573
19	70	17.1	132	4	US-09-651-236-573
20	69	16.9	71	4	US-09-513-999C-6619
21	68	16.6	73	4	US-09-513-999C-4484
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23	67	16.4	99	4	US-09-621-976-6393
24	66	16.1	91	4	US-09-621-976-5929
25	64.5	15.8	375	2	US-08-454-557C-121
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27	64.5	15.8	375	2	US-08-450-673C-121

Sequence 2, Appli
Sequence 6835, Ap
Sequence 6836, Ap
Sequence 6837, Ap
Sequence 5592, Ap
Sequence 56714, A
Sequence 41493, A
Sequence 12, Appl
Sequence 42537, A
Sequence 6178, Ap
Sequence 6275, Ap
Sequence 6678, Ap
Sequence 6761, Ap
Sequence 6763, Ap
Sequence 6778, Ap
Sequence 6813, Ap
Sequence 6816, Ap
Sequence 6817, Ap

28 64.5 15.8 375 4 US-09-872-968-2
29 63 15.4 51 4 US-09-513-999C-6835
30 63 15.4 54 4 US-09-513-999C-6836
31 63 15.4 54 4 US-09-513-999C-6837
32 62 15.2 120 4 US-09-621-976-5592
33 62 15.2 179 4 US-09-270-767-56714
34 62 15.2 396 4 US-09-270-767-41493
35 60 14.7 727 4 US-09-445-023A-12
36 59.5 14.5 400 4 US-09-270-767-42537
37 59 14.4 56 4 US-09-621-976-6178
38 59 14.4 56 4 US-09-621-976-6275
39 59 14.4 56 4 US-09-621-976-6678
40 59 14.4 56 4 US-09-621-976-6761
41 59 14.4 56 4 US-09-621-976-6763
42 59 14.4 56 4 US-09-621-976-6778
43 59 14.4 56 4 US-09-621-976-6813
44 59 14.4 56 4 US-09-621-976-6816
45 59 14.4 56 4 US-09-621-976-6817

ALIGNMENTS

RESULT 1

US-08-454-557C-48
; Sequence 48, Application US/08454557C
; Patent No. 5830670
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,557C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 75 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

US-08-454-557C-48
Query Match 100.0%; Score 409; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.8e-46;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SSSLGPKCWDYRHELLSLALMINFRVWACTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
Db 1 SSSLGPKCWDYRHELLSLALMINFRVWACTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
Qy 61 ALLTINGHCTWLPAS 75


```
; LENGTH: 75 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US95-17111A-48

Query Match 100.0%; Score 409; DB 5; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.8e-46; Indels 0; Gaps 0;
Matches 75; Conservative 0; Mismatches 0;

Qy 1 SSSGLPKCWDYRHELLSLALMINFRVMACCTFKQHIELROKISIVPRKLCMGVCPVKI 60
Db 1 SSSGLPKCWDYRHELLSLALMINFRVMACCTFKQHIELROKISIVPRKLCMGVCPVKI 60

Qy 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 5
US-09-227-357-578
; Sequence 578, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950

; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-578

Query Match 21.0%; Score 86; DB 3; Length 72;
Best Local Similarity 75.0%; Pred. No. 0.00061;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSSGLPKCWDYRHELLSLA 20
Db 1 STHGLPCWDYRHEPLCLA 20

RESULT 6
US-09-513-999C-7795
; Sequence 7795, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7795
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 35
; OTHER INFORMATION: Xaa= * or Glu or Gln
US-09-513-999C-7795

Query Match 19.9%; Score 81.5; DB 4; Length 55;
Best Local Similarity 51.5%; Pred. No. 0.0017;
Matches 17; Conservative 2; Mismatches 11; Indels 3; Gaps 1;

Qy 1 SSSGLPKCWDYRHE---LLSLALMINFRVMAC 30
Db 19 SSCLSLPKCWDYRHEPCAPLPFSSESFRISDC 51
```

RESULT 7
US-09-513-999C-5298
; Sequence 5298, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2.98
; CURRENT APPLICATION NUMBER: US/09/513.999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5298
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5298

Query Match 18.5%; Score 75.5; DB 4; Length 82;
Best Local Similarity 55.2%; Pred. No. 0.017;
Matches 16; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 5 GLEKCDYRHELLSLALMINFRVWACTFK 33
|:|||||||:|||||:|

Db 54 GIPKCDYRQEPRLALIVLSVVV-AFK 81
|:|||||||:|||||:|

RESULT 8
US-09-685-166A-884
; Sequence 884, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685.166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 884
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-685-166A-884

Query Match 17.8%; Score 73; DB 4; Length 135;
Best Local Similarity 48.3%; Pred. No. 0.065;
Matches 14; Conservative 7; Mismatches 6; Indels 2; Gaps 1;

QY 1 SSSLGLPKCDYRHELLSLA--LMINFRV 27
|:|||||||:|||||:|

Db 106 SACLGLPKCWYRHKPPHPACHILLNYQV 134
|:|||||||:|||||:|

RESULT 9
US-09-679-426-884
; Sequence 884, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679.426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 884
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-679-426-884

Query Match 17.8%; Score 73; DB 4; Length 135;
Best Local Similarity 48.3%; Pred. No. 0.065;
Matches 14; Conservative 7; Mismatches 6; Indels 2; Gaps 1;

QY 1 SSSLGLPKCWYRHELLSLA--LMINFRV 27
|:|||||||:|||||:|

Db 106 SACLGLPKCWYRHKPPHPACHILLNYQV 134
|:|||||||:|||||:|

RESULT 10
US-09-759-143-884
; Sequence 884, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23

; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
; TITLE OF INVENTION: Detection of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17111A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,426
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-17111A-121

Query Match 17.5%; Score 71.5; DB 5; Length 397;
Best Local Similarity 28.2%; Pred. No. 0.36; Mismatches 29; Indels 23; Gaps 3;
Matches 24; Conservative 9;
QY 1 SSSLGLPKCWDYRHLLSLALMIFRMVAC-----TFKHTELROKISIVPR 47
Db 119 STCLSLPKCWDYRAAVPGILFFLRLHRCPTLTQDEVQWCDHSLQPSLIRSSI-LLPQ 177
QY 48 KLCCMGFVCPVKIALTLINGHCTWL 72
Db 178 -----PPKVAGTKDMHHTWL 193

RESULT 15
US-09-636-215-573
; Sequence 573, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 573
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-215-573
Query Match 17.1%; Score 70; DB 4; Length 132;
Best Local Similarity 73.3%; Pred. No. 0.16; Mismatches 2; Indels 0; Gaps 0;
Matches 11; Conservative 2;
QY 1 SSSLGLPKCWDYRHE 15
Db 106 SACLGLPKCMGYRHK 120
Search completed: October 11, 2005, 07:42:51
Job time : 18.1457 secs

T49191
hypothetical protein MAA21.130 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #tes
C:Accession: T49191
R:Rieger, M.; Mueller-Auer, S.; Zipf, M.; Schaefer, M.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25018
A:Accession: T49191
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1162 <R16>
A:Cross-references: UNIPROT:Q9LYK5; EMBL:AL163818; GSP
A:Experimental source: cultivar Columbia; BAC clone MA
C:Genetics:
A:Gene: ATSP:MAA21.130
A:Map position: 3
A:Introns: 975/1

C;Superfamily: Arabidopsis thaliana hypothetical protein MAA21.130

Query Match 16.2%; Score 63.5; DB 2; Length 1162;
Best Local Similarity 28.9%; Pred. No. 20;
Matches 22; Conservative 4; Mismatches 23; Indels 27; Gaps 5;

QY 13 IKGNSSFFLLSFFFS-----FQN-----C-----CQCFCRTTEGYAVECFY 50
Db 779 LKSGRDFLLDINSISSHLAEIFMNMCKNLSCRILLPVDECDRCVCRKDGFCACM- 837

QY 51 CLV-----DKAAFECSW 62
Db 838 CLVCSNPFDMASNTCSW 853

RESULT 3

E84611
hypothetical protein At2g2340 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: E84611
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84611
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-358 <STO>
A;Cross-references: UNIPROT:Q9SJZ9; GB:AF002093; NID:g4544455; PIDN:AAD22363.1; GSPDB:GN

Query Match 15.9%; Score 62.5; DB 2; Length 358;
Best Local Similarity 24.7%; Pred. No. 10;
Matches 18; Conservative 10; Mismatches 20; Indels 25; Gaps 3;
QY 2 FVCLILNRKIKGNSSFFLL-----SFFSFQNCQCFCRTTEGYAVECFYC 51
Db 294 FIYMTANYEVYKGRNRFYLACKASDQAWSIPLLYRNCYQ-----FLL 339
QY 52 LVDKAAFECSW 64
Db 340 FVSMVVE-WFIY 351

RESULT 4

T11074
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - nematode (Onchocerca volvulus) m
C;Species: mitochondrion Onchocerca volvulus
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T11074
R;Keddie, E.M.; Higazi, T.; Unnasch, T.R.
Mol. Biochem. Parasitol. 95, 111-127, 1998
A;Title: The mitochondrial genome of Onchocerca volvulus: Sequence, structure and phylog
A;Reference number: T17246; MUID:98434257; PMID:9763293
A;Accession: T11074
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-531 <KED>
A;Cross-references: UNIPROT:O47582; EMBL:AF015193; NID:g2735934; PID:g2735946; PIDN:AA06
A;Experimental source: strain forest
C;Genetics:
A;Genome: mitochondrion
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 15.9%; Score 62.5; DB 2; Length 531;
Best Local Similarity 22.2%; Pred. No. 14;
Matches 14; Conservative 11; Mismatches 21; Indels 17; Gaps 2;

QY 20 FLLSFFF--SFQNCQCFCQ-----RTTEGYAVECFYCLVDKAAFECSW 62
Db 361 FFLVPFVFGVELTFCYCYRMFFLPRVGAFGPDYVGFSSKLFYFSCFFLVFVFSVWFTFW 420
QY 63 FYS 65
Db 421 VFS 423

RESULT 5

T17625
hypothetical protein A135L - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17625
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806
A;Accession: T17625
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-182 <GRA>

A;Cross-references: UNIPROT:Q84455; EMBL:U42580; NID:g4028896; PIDN:AAC96503.1
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Note: A135L

Query Match 15.8%; Score 62; DB 2; Length 182;
Best Local Similarity 28.0%; Pred. No. 6.7;
Matches 14; Conservative 10; Mismatches 22; Indels 4; Gaps 2;

QY 18 SSFF--LLSFFSFQNCQCFCQRTTEGYAVECFYCLVDKAAFECSW 65
Db 30 TSFFFAFIDFFIAFRKAFACAFCAISAGFTV--FFIFLAFSSAMWFFS 77

RESULT 6

T48167
hypothetical protein T1008.160 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48167
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, K.
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24486
A;Accession: T48167
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-428 <BEV>

A;Cross-references: UNIPROT:Q9M029; EMBL:AL161746
A;Experimental source: cultivar Columbia; BAC clone T1008
C;Genetics:
A;Map position: 5
A;Introns: 85/2; 100/3; 142/3; 174/1; 203/2; 229/3; 278/3; 303/1; 404/2
A;Note: T1008.160

Query Match 15.8%; Score 62; DB 2; Length 428;
Best Local Similarity 29.5%; Pred. No. 13;
Matches 18; Conservative 9; Mismatches 16; Indels 18; Gaps 3;

QY 6 LILNREKIKG-----GNSFFLL-----SFFSFQNCQCFCQRT-----TEGYAVE 47
Db 355 ILTSTELSGANGEGHSHSTRYLCAICYDAPRDCFFLSCGHCVCACFOGTRIETSQFCPV 414

QY 48 C 48
Db 415 C 415

RESULT 7

T21630
hypothetical protein F32B4.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21630
R;White, S.
Submitted to the EMBL Data Library, November 1996
A;Reference number: Z19452
A;Accession: T21630
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-277 <WIL>
A;Cross-references: UNIPROT:O62200; EMBL:Z81522; PIDN:CAB04230.1; GSPDB:GN00019; CESP:F3324
A;Gene: CESP:F32B4.5
C;Genetics:
A;Map position: 1
A;Introns: 131/3; 237/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F32B4.5

Query Match 15.6%; Score 61.5; DB 2; Length 277;
Best Local Similarity 63.6%; Pred. No. 11;
Matches 14; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 9 NREKIKGNSS-FLLSFFPSF 29
DB 190 NPEPVKGTTSPPFLSFFFPF 211

RESULT 8
S64041
probable membrane protein YGL039w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein G3620
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: S64041
R;Hebling, U.; Hofmann, B.; Delius, H.
Submitted to the Protein Sequence Database, May 1996
A;Reference number: S64003
A;Accession: S64041
A;Molecule type: DNA
A;Residues: 1-348 <HEB>
A;Cross-references: UNIPROT:P53183; EMBL:Z72561; NID:gl322521; PID:gl322522; GSPDB:GN00040
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YGL039w
A;Cross-references: SGD:S0003007
A;Map position: 7L
C;Superfamily: dihydrokaempferol 4-reductase
C;Keywords: transmembrane protein
F;6-22/Domain: transmembrane #status predicted <TMM>

Query Match 15.6%; Score 61.5; DB 2; Length 348;
Best Local Similarity 31.9%; Pred. No. 13;
Matches 23; Conservative 10; Mismatches 16; Indels 23; Gaps 6;

QY 3 VFCL-----ILNRE--KIKG-----GNSSFFLLSFFPSFQCCQCFCRTTE--GVAV 46
DB 274 MFCQEQALDIINEFPOLKGIATGPGSGTFLT-----KNCKCDNRKTNLLGFQF 327

QY 47 ECFY-CLVDKAA 57
DB 328 NKFRDCIVDTAS 339

RESULT 9
D71351
probable primosomal protein N (p18A) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: D71351
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998

C;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: D71351
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-657 <COL>
A;Cross-references: UNIPROT:O81258; GB:AE001204; GB:AE000520; NID:g3322492; PIDN:AAC6521
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0230

Query Match 15.6%; Score 61.5; DB 2; Length 657;
Best Local Similarity 30.0%; Pred. No. 22;
Matches 24; Conservative 8; Mismatches 23; Indels 25; Gaps 4;

QY 8 LNREKIKGNSSFFLLSFFPSFQCCQCFCRTTEG-----AVECF 49
DB 341 IRKTEAGYQSMFLNRRGFSYS-----FQCRSC-GYTLCCTQCAVPLTWHKRVGAMQCH 394

QY 50 YCLVDKAAFE-CWVFYSFDT 68
DB 395 YCGRQAPPEPCPCCHSFT 414

RESULT 10
S45981
probable membrane protein YBR113w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR0908E
C;Species: Saccharomyces cerevisiae
C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: S45981
R;Feldmann, H.; Mannhaupt, G.; Schwarzlouse, C.; Vetter, I.
Submitted to the Protein Sequence Database, August 1994
A;Reference number: S45927
A;Accession: S45981
A;Molecule type: DNA
A;Residues: 1-160 <FEL>
A;Cross-references: UNIPROT:P38267; EMBL:Z35981; NID:G536449; PID:G536451; GSPDB:GN000002
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YBR113w
A;Cross-references: SGD:S0000317
A;Map position: 2R
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YBR113w
C;Keywords: transmembrane protein
F;32-64/Domain: transmembrane #status predicted <TM1>
F;67-89/Domain: transmembrane #status predicted <TM2>
F;113-142/Domain: transmembrane #status predicted <TM3>

Query Match 15.5%; Score 61; DB 2; Length 160;
Best Local Similarity 48.4%; Pred. No. 7.9;
Matches 15; Conservative 4; Mismatches 10; Indels 2; Gaps 2;

QY 19 SFLLSFFPS-FQNCQCFCRTT-EGYAVE 47
DB 68 SFLLIFFQSCFVCCCCSCCSLSLKAYSSE 98

RESULT 11
AC2432
hypothetical protein all5011 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Status: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AC2432
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
baena sp. strain PCC 7120
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC2432
A;Status: preliminary
A;Molecule type: DNA

Search completed: October 11, 2005, 07:01:40
Job time : 11.5455 secs

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Query Match      15.1%   Score 59.5; DB 2; Length 274;
Best Local Similarity 39.6%; Pred. NO. 18;
Matches 19; Conservative 5; Mismatches 15; Indels 9; Gaps 3;
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```
Qy    22 LLSPFFSFQNCCQFCQRTTGGYAVECFYCIVDKAAECWMFYS-FDT 68
       :         :          :           :             :
Db     120 LPSNFFFXGE---EGCQCKGAKYTVEC-----AQAAFSDRGFIPLFDI 159
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 40.8182 Seconds
(without alignments)
853.085 Million cell updates/sec

Title: US-10-092-934-8
Perfect score: 393
Sequence: 1 MFVFCILLNREKINGNSSP.....FYCLVDKAAPECWFFYSFDT 68

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74.5	19.0	462	2 Q75FL9	Q75FL9 leptospira
2	74.5	19.0	462	2 Q8EXK1	Q8EXK1 leptospira
3	70.5	17.9	2063	2 Q7ROU1	Q7ROU1 plasmodium
4	69	17.6	168	2 Q6YQ78	Q6YQ78 onion yello
5	67.5	17.2	1116	2 Q7FA22	Q7FA22 oryza sativ
6	67	17.0	133	2 Q8FL93	Q8FL93 candida gla
7	66.5	16.9	131	1 CD59_SAI5C	P47777 salmieri sci
8	66	16.8	122	2 Q6MSW2	Q6MSW2 mycoplasma
9	66	16.8	275	2 Q8S204	Q8S204 oryza sativ
10	65	16.5	304	2 Q894Q5	Q894Q5 clostidium
11	64.5	16.4	834	2 Q9IC56	Q9IC56 hepatitis b
12	64	16.3	1798	2 Q6ZM73	Q6ZM73 brachydanio
13	63.5	16.2	144	2 Q97454	Q97454 drosophila
14	63.5	16.2	975	2 Q84T13	Q84T13 arabidopsis
15	63.5	16.2	1162	2 Q8LY65	Q8LY65 arabidopsis
16	63	16.0	128	1 CD59_AOTTR	P51447 actus trivi
17	62.5	15.9	358	2 Q9SJZ9	Q9SJZ9 arabidopsis
18	62.5	15.9	531	2 Q47582	Q47582 onchocerca
19	62.5	15.9	531	2 Q70UR6	Q70UR6 dirofilaria
20	62.5	15.9	734	1 CD97_BOVIN	Q8AQA4 bos taurus
21	62.5	15.9	827	2 Q702T4	Q702T4 bos taurus
22	62	15.8	182	2 Q84455	Q84455 paramacium
23	62	15.8	428	2 Q9M029	Q9M029 arabidopsis
24	62	15.8	444	2 Q6DBH0	Q6DBH0 arabidopsis
25	62	15.8	844	2 Q8C804	Q8C804 mus musculu
26	62	15.8	1912	2 Q95226	Q95226 homo sapien
27	62	15.8	1966	1 CCAF_HUMAN	Q60840 homo sapien
28	62	15.8	1977	2 Q9UHB1	Q9UHB1 homo sapien
29	62	15.8	1981	2 Q92327	Q92327 rattus norv
30	62	15.8	1984	2 Q7TNT3	Q7TNT3 mus musculu
31	62	15.8	1985	1 CCAF_MOUSE	Q9JIS7 mus musculu

32	61.5	15.6	277	2 O62200	O62200 caenorhabdi
33	61.5	15.6	348	1 YGD9_YEAST	P53183 saccharomyc
34	61.5	15.6	657	1 PRIA_TREPA	O83258 treponema p
35	61.5	15.6	838	2 Q9IC47	Q9IC47 hepatitis b
36	61	15.5	128	1 CD59_CALSQ	P46657 callithrix
37	61	15.5	160	1 YBW3_YEAST	P38267 saccharomyc
38	61	15.5	231	2 Q8I3X1	Q8I3X1 plasmodium
39	61	15.5	234	2 Q8JJP7	O8JJP7 porcine lym
40	61	15.5	320	2 Q8YMC3	Q8YMC3 anabaena sp
41	60.5	15.4	780	2 Q9WFE1	Q9WFE1 hepatitis b
42	60.5	15.4	5179	1 MUC2_HUMAN	Q02817 homo sapien
43	60	15.3	80	2 O21898	O21898 bacterioph
44	60	15.3	324	2 Q22283	Q22283 caenorhabdi
45	60	15.3	431	2 Q8XXQ6	Q8XXQ6 talstonia s

ALIGNMENTS

RESULT 1

ID	Q75FL9	PRELIMINARY;	PRT;	462 AA.
AC	Q75FL9;			
DT	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DE	Hypothetical protein.			
GN	OrderedLocusNames=LIC20163;			
OS	Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar Copenhageni).			
OC	Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.			
OX	NCBI_TaxID=44275;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Fiocruz L1-130;			
RX	PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;			
RA	Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B., Ho P.L., Haake D.A., Verjovski-Almeida S., Hartskeerl R.A., Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H., Coutinho L.L., Degraeve W.M., Dellagostin O.A., El-Dorfi H., Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Giglioti E.A., Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R., Jeronimo S.M.B., Junqueira-de-Azevedo J.L.M., Kimura E.T., Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R., de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A., Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A., Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.; "Comparative genomics of two Leptospira interrogans serovars reveals novel insights into physiology and pathogenesis."; J. Bacteriol. 186:2164-2172(2004).			
RL	EMBL; AE016824; AAS72191.1; -.			
KW	Complete proteome.			
SQ	SEQUENCE 462 AA; 54921 MW; 2FD430227AEC35F0 CRC64;			

Query Match 19.0%; Score 74.5; DB 2; Length 462;
Best Local Similarity 26.5%; Pred. No. 1.9;
Matches 22; Conservative 12; Mismatches 20; Indels 29; Gaps 4;

Qy	8 LNREKIKGG-----NSSFFLL---SFFSFONCCQCFQCRTEGVAV 46
Db	286 LNFGEVGNGLRVLRHLSWEQRESLPYLNLTFWILFCTFFFNPKNIWKRFQIET-----I 340
Qy	47 ECFYCLVDKAAFECEW---FYSF 66
Db	341 LLLFWLPSILFYTWEGYFEEF 363

RESULT 2

ID	Q8EXK1	PRELIMINARY;	PRT;	462 AA.
AC	Q8EXK1;			
DT	01-MAR-2003 (TrEMBLrel. 23, Created)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)			

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DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=LB207;
OS Leptospora interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AE011608; AAN51766.1; -.
KW Complete proteome.
SQ SEQUENCE 462 AA; 54887 MW; AFE8659C2B986B4C CRC64;

Query Match 19.0%; Score 74.5; DB 2; Length 462;
Best Local Similarity 26.5%; Pred. No. 1.9;
Matches 22; Conservative 12; Mismatches 20; Indels 29; Gaps 4;

QY 8 LNREKIKGG-----NSSFFLL--SFFSFQNCQCQCQTTEGYAV 46
DB 286 LNFEGVNGVRUHLHSWEQRESLYNLNLTFWILFCTFFFPKNWRFQIET-----I 340
QY 47 ECFYCLVDKAAFCW---FYSF 66
DB 341 LLLFWLIPSLFYTWEGYFEF 363

RESULT 3
Q7RQL1
ID Q7RQL1 PRELIMINARY; PRT; 2063 AA.
AC Q7RQL1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Myosin heavy chain.
GN Name=PY01085;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteza M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.B.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL0100287; EAA20190.1; -.
DR HSSP; Q02440; 10E9
DR GO; GO:0016459; C:myosin; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
```

```
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR001451; Hexapep.transf.
DR InterPro; IPR001609; Myosin.head.
DR InterPro; IPR002078; Sig54.interact.
DR Pfam; PF00063; Myosin.head; 5.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; Myosin.head; 1.
DR PROSITE; PS00101; HEXAPEP.TRANSFERASES; UNKNOWN_2.
DR PROSITE; PS00675; SIGWAS4.INTERACT.1; 1.
SQ SEQUENCE 2063 AA; 240303 MW; 4DCB8E3B8E7D2ABA CRC64;

Query Match 17.9%; Score 70.5; DB 2; Length 2063;
Best Local Similarity 30.6%; Pred. No. 21;
Matches 19; Conservative 10; Mismatches 28; Indels 5; Gaps 2;

QY 7 ILNREKIKGNSFFLLSFFSFQNCQCQCQTTEGYAVECFYCLVDKAAFCWPFYSF 66
DB 1095 IVNKNKIKINES----IKOFFNPFYNCCKPYAI-CTKGYENLCYTSFAKRLTMGSDIFQSI 1149
QY 67 DT 68
DB 1150 ET 1151

RESULT 4
Q6YQ78
ID Q6YQ78 PRELIMINARY; PRT; 168 AA.
AC Q6YQ78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
GN OrderedLocusNames=PAM497;
OS Onion yellows phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Candidatus Phytoplasma.
OX NCBI_TaxID=100379;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OY-M;
RX PubMed=14661021; DOI=10.1038/ng1277;
RA Oshima K., Kakizawa S., Nishigawa H., Jung H.-Y., Wei W., Suzuki S.,
RA Arashida R., Nakata D., Miyata S.-I., Ugaki M., Namba S.;
RT "Reductive evolution suggested from the complete genome sequence of a
RT plant-pathogenic phytoplasma.";
RL Nat. Genet. 36:27-29(2004).
DR EMBL; AF006628; BAD04582.1; -.
KW Complete proteome.
SQ SEQUENCE 168 AA; 19313 MW; D7038A05C94A149E CRC64;

Query Match 17.6%; Score 69; DB 2; Length 168;
Best Local Similarity 33.9%; Pred. No. 3.4;
Matches 19; Conservative 5; Mismatches 16; Indels 16; Gaps 4;

QY 19 SFFLLSFFSFQNCQCQCQCQTTEGYAVECFY-----CLVDKAAFCW----WFYS 65
DB 27 NFFSFFFSY-----CPSCCIISFGSG--CSYFSFNSCATISKFNCFYVKLWFSS 75

RESULT 5
Q7FAF2
ID Q7FAF2 PRELIMINARY; PRT; 1116 AA.
AC Q7FAF2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE OSJNB0026E15.4 protein.
GN Name=OSJNB0026E15.4;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
```

OC Ehrhartoideae; Oryzeae; Oryza.
 ON NCBI_TaxID=39947;
 RN
 RP SEQUENCE FROM N.A.
 RX PubMed=12447439; DOI=10.1038/nature01183;
 RA Peng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
 RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
 RA Wang Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
 RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
 RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
 RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
 RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
 RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
 RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
 RA Han B.;
 RT "Sequence and analysis of rice chromosome 4.";
 RL Nature 420:316-320(2002).
 DR ENBL; AL607008; CAE03686.2; -;
 DR InterPro; IPR009085; Hde.
 DR InterPro; IPR004332; MuDR.
 DR InterPro; IPR001156; Peptidase_S60.
 DR InterPro; IPR007527; Znf_SWIM.
 DR Pfam; PF03108; MuDR; 1.
 DR Pfam; PF04434; SWIM; 1.
 DR PROSITE; PS00205; TRANSFERRIN_1; UNKNOWN 1.
 SQ SEQUENCE 1116 AA; 127501 MW; 991D6E3CE981802E CRC64;
 Query Match 17.2%; Score 67.5; DB 2; Length 1116;
 Best Local Similarity 25.4%; Pred. No. 27;
 Matches 18; Conservative 13; Mismatches 27; Indels 13; Gaps 4;
 QY 4 FCUILNREKIKGNSFFLLSP--FFSFQNCOCFCQRT-----TEGVAVEFCYCLV 53
 Db 387 YVAVQNRSIRPN--YFVQWAFAGACIHAFCQSRMLCVDVAGDKPIIPVAFGV 444
 QY 54 DXAAPECW-WF 63
 Db 445 ESENYESLWF 455
 RESULT 6
 Q6FL93 PRELIMINARY; PRT; 133 AA.
 ID Q6FL93 AC Q6FL93;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Similarity.
 GN ORFNames=CAGL01052149;
 OS Candida glabrata CBS138.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 ON NCBI_TaxID=284593;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS138;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anchaud V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boissame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
 RA Depons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jaumiaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swennene D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts.";
 RL Nature 430:35-44(2004).
 DR ENBL; CR380958; CAG61971.1; -;
 SQ SEQUENCE 133 AA; 15668 MW; C2CA08223BE312A1 CRC64;
 Query Match 17.0%; Score 67; DB 2; Length 133;
 Best Local Similarity 28.2%; Pred. No. 4.7;
 Matches 20; Conservative 10; Mismatches 31; Indels 10; Gaps 2;
 QY 1 MFVFCILINREKIKGNSFFLLSP-----FFSFQNCOCFCQRTTEGVAVEFCYCLVDKA 56
 Db 41 LLAICLLLHTRKPHLQSHAFNYFSISLLFFDFENSILCVTIQTYVYVCACYLLFYRG 100
 QY 57 APECMWFYSFD 67
 Db 101 -----FHLFD 105
 RESULT 7
 CD59 SAISC STANDARD; PRT; 131 AA.
 ID_CD59 SAISC AC P47777;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE CD59 glycoprotein precursor (Membrane attack complex inhibition factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
 DE Name=CD59;
 GN Saimiri sciureus (Common squirrel monkey).
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
 ON NCBI_TaxID=9521;
 RN
 RP SEQUENCE FROM N.A.
 RX TISSUE=Lung;
 RC MEDLINE=94118421; PubMed=7507185;
 RA Rother R.P., Rollins S.A., Fodor W.L., Albrecht J.C., Setter E.,
 RA Fleckenstein B., Quinto S.P.;
 RT "Inhibition of complement-mediated cytolysis by the terminal complement inhibitor of herpesvirus saimiri.";
 RL J. Virol. 68:730-737(1994).
 CC -!- FUNCTION: Potent inhibitor of the complement membrane attack complex (MAC) action. Acts at or after the C5b-8 stage of MAC assembly.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).
 CC -!- SIMILARITY: Contains 1 UPAR/Ly6 domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcement or send an email to license@isb-sib.ch).
 DR ENBL; L22859; AAA16747.1; -;
 DR PIR; I56894; I56894.
 DR HSP; P13987; LCDS.
 DR InterPro; IPR003632; Ly-6_CD59.
 DR InterPro; IPR001526; Ly6_UPAR.
 DR Pfam; PF00021; UPAR_Ly6; 1.
 DR ProDom; PD003128; Ly-6_CD59; 1.
 DR SMART; SM00134; LU; 1.
 DR PROSITE; PS00983; Ly6_UPAR; FALSE NEG.
 KW Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.
 ST SIGNAL 1 25 By similarity.
 FT CHAIN 26 105 CD59 glycoprotein.
 FT PROPEP 106 131 Removed in mature form (By similarity).
 FT DOMAIN 26 111 UPAR/Ly6.
 FT DISULFID 28 54 By similarity.
 FT DISULFID 31 41 By similarity.
 FT DISULFID 47 67 By similarity.
 FT DISULFID 73 91 By similarity.
 FT DISULFID 92 97 By similarity.

DR ENBL; CR380958; CAG61971.1; -. C2CA08223BE312A1 CRC64;
SQ SEQUENCE 133 AA; 15666 MW; 2

Query Match 17.0%; Score 67; DB 2; Length 133;
Best Local Similarity 28.2%; Pred. No. 4.7;
Matches 20; Conservative 10; Mismatches 31; Indels 10; Gaps 2

QY 1 MFVFCILINREKIKGNSFFLLSP-----FFSFQNCOCFCQRTTTEGVAVEFCYCLV 56
DB 41 LLAICLLHLTKPHLQSHAFNYFSISLLFFDFENSILCVTIQTYVYVCACYLLFYRG 100
QY 57 APECWMFYSD 67
DB 101 -----FHLFD 105

RESULT 7
CD59_SAISC STANDARD; PRT; 131 AA.
ID_CD59_SAISC STANDARD; PRT; 131 AA.
AC P47777;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE CD59 glycoprotein precursor (Membrane attack complex inhibition factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
DE Name=CD59;
GN Saimiri sciureus (Common squirrel monkey).
OS Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
RC MEDLINE=94118421; PubMed=7507185;
RA Rother R.P., Rollins S.A., Fodor W.L., Albrecht J.-C., Setter E.,
RA Fleckenstein B., Quinto S.P.,
RT "Inhibition of complement-mediated cytolysis by the terminal
complement inhibitor of herpesvirus saimiri.";
RL J. Virol. 68:730-737(1994).
CC -!- FUNCTION: Potent inhibitor of the complement membrane attack
complex (MAC) action. Acts at or after the C5b-8 stage of MAC
assembly.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
similarity).
CC -!- SIMILARITY: Contains 1 UPAR/Ly6 domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announcement>
or send an email to license@isb-sib.ch).
CC
DR ENBL; L22859; AAA16747.1; -.
DR PIR; I56894; I56894.
DR HSP; P13987; LCDS.
DR InterPro; IPR003632; Ly-6 CD59.
DR InterPro; IPR001526; Ly6_UPAR.
DR Pfam; PF00021; UPAR_Ly6; 1.
DR ProDom; PD003128; Ly-6_CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; Ly6 UPAR; FALSE NEG.
KW Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.
STIGNAL 1 25 By similarity.
FT CHAIN 26 105 CD59 glycoprotein.
FT PROPEP 106 131 Removed in mature form (By similarity).
FT DOMAIN 26 111 UPAR/Ly6.
FT DISULFID 28 54 By similarity.
FT DISULFID 31 41 By similarity.
FT DISULFID 47 67 By similarity.
FT DISULFID 73 91 By similarity.
FT DISULFID 92 97 By similarity.

DR ENBL; L22859; AAA16747.1; -.
DR PIR; I56894; I56894.
DR HSP; P13987; LCDS.
DR InterPro; IPR003632; Ly-6 CD59.
DR InterPro; IPR001526; Ly6_UPAR.
DR Pfam; PF00021; UPAR_Ly6; 1.
DR ProDom; PD003128; Ly-6_CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; Ly6 UPAR; FALSE NEG.
KW Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.
STIGNAL 1 25 By similarity.
FT CHAIN 26 105 CD59 glycoprotein.
FT PROPEP 106 131 Removed in mature form (By similarity).
FT DOMAIN 26 111 UPAR/Ly6.
FT DISULFID 28 54 By similarity.
FT DISULFID 31 41 By similarity.
FT DISULFID 47 67 By similarity.
FT DISULFID 73 91 By similarity.
FT DISULFID 92 97 By similarity.

DR ENBL; L22859; AAA16747.1; -.
DR PIR; I56894; I56894.
DR HSP; P13987; LCDS.
DR InterPro; IPR003632; Ly-6 CD59.
DR InterPro; IPR001526; Ly6_UPAR.
DR Pfam; PF00021; UPAR_Ly6; 1.
DR ProDom; PD003128; Ly-6_CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; Ly6 UPAR; FALSE NEG.
KW Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.
STIGNAL 1 25 By similarity.
FT CHAIN 26 105 CD59 glycoprotein.
FT PROPEP 106 131 Removed in mature form (By similarity).
FT DOMAIN 26 111 UPAR/Ly6.
FT DISULFID 28 54 By similarity.
FT DISULFID 31 41 By similarity.
FT DISULFID 47 67 By similarity.
FT DISULFID 73 91 By similarity.
FT DISULFID 92 97 By similarity.

DR ENBL; L22859; AAA16747.1; -.
DR PIR; I56894; I56894.
DR HSP; P13987; LCDS.
DR InterPro; IPR003632; Ly-6 CD59.
DR InterPro; IPR001526; Ly6_UPAR.
DR Pfam; PF00021; UPAR_Ly6; 1.
DR ProDom; PD003128; Ly-6_CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; Ly6 UPAR; FALSE NEG.
KW Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.
STIGNAL 1 25 By similarity.
FT CHAIN 26 105 CD59 glycoprotein.
FT PROPEP 106 131 Removed in mature form (By similarity).
FT DOMAIN 26 111 UPAR/Ly6.
FT DISULFID 28 54 By similarity.
FT DISULFID 31 41 By similarity.
FT DISULFID 47 67 By similarity.
FT DISULFID 73 91 By similarity.
FT DISULFID 92 97 By similarity.

DR ENBL; L22859; AAA16747.1; -.
DR PIR; I56894; I56894.
DR HSP; P13987; LCDS.
DR InterPro; IPR003632; Ly-6 CD59.
DR InterPro; IPR001526; Ly6_UPAR.
DR Pfam; PF00021; UPAR_Ly6; 1.
DR ProDom; PD003128; Ly-6_CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; Ly6 UPAR; FALSE NEG.
KW Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.
STIGNAL 1 25 By similarity.
FT CHAIN 26 105 CD59 glycoprotein.
FT PROPEP 106 131 Removed in mature form (By similarity).
FT DOMAIN 26 111 UPAR/Ly6.
FT DISULFID 28 54 By similarity.
FT DISULFID 31 41 By similarity.
FT DISULFID 47 67 By similarity.
FT DISULFID 73 91 By similarity.
FT DISULFID 92 97 By similarity.

DR ENBL; L22859; AAA16747.1; -.
DR PIR; I56894; I56894.
DR HSP; P13987; LCDS.
DR InterPro; IPR003632; Ly-6 CD59.
DR InterPro; IPR001526; Ly6_UPAR.
DR Pfam; PF00021; UPAR_Ly6; 1.
DR ProDom; PD003128; Ly-6_CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; Ly6 UPAR; FALSE NEG.
KW Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.
STIGNAL 1 25 By similarity.
FT CHAIN 26 105 CD59 glycoprotein.
FT PROPEP 106 131 Removed in mature form (By similarity).
FT DOMAIN 26 111 UPAR/Ly6.
FT DISULFID 28 54 By similarity.
FT DISULFID 31 41 By similarity.
FT DISULFID 47 67 By similarity.
FT DISULFID 73 91 By similarity.
FT DISULFID 92 97 By similarity.

DR ENBL; L22859; AAA16747.1; -.
DR PIR; I56894; I56894.
DR HSP; P13987; LCDS.
DR InterPro; IPR003632; Ly-6 CD59.
DR InterPro; IPR001526; Ly6_UPAR.
DR Pfam; PF00021; UPAR_Ly6; 1.
DR ProDom; PD003128; Ly-6_CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; Ly6 UPAR; FALSE NEG.
KW Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.
STIGNAL 1 25 By similarity.
FT CHAIN 26 105 CD59 glycoprotein.
FT PROPEP 106 131 Removed in mature form (By similarity).
FT DOMAIN 26 111 UPAR/Ly6.
FT DISULFID 28 54 By similarity.
FT DISULFID 31 41 By similarity.
FT DISULFID 47 67 By similarity.
FT DISULFID 73 91 By similarity.
FT DISULFID 92 97 By similarity.

DR ENBL; L22859; AAA16747.1; -.
DR PIR; I56894; I56894.
DR HSP; P13987; LCDS.
DR InterPro; IPR003632; Ly-6 CD59.
DR InterPro; IPR001526; Ly6_UPAR.
DR Pfam; PF00021; UPAR_Ly6; 1.
DR ProDom; PD003128; Ly-6_CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; Ly6 UPAR; FALSE NEG.
KW Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.
STIGNAL 1 25 By similarity.
FT CHAIN 26 105 CD59 glycoprotein.
FT PROPEP 106 131 Removed in mature form (By similarity).
FT DOMAIN 26 111 UPAR/Ly6.
FT DISULFID 28 54 By similarity.
FT DISULFID 31 41 By similarity.
FT DISULFID 47 67 By similarity.
FT DISULFID 73 91 By similarity.
FT DISULFID 92 97 By similarity.

DR ENBL; L22859; AAA16747.1; -.
DR PIR; I56894; I56894.
DR HSP; P13987; LCDS.
DR InterPro; IPR003632; Ly-6 CD59.
DR InterPro; IPR001526; Ly6_UPAR.
DR Pfam; PF00021; UPAR_Ly6; 1.
DR ProDom; PD003128; Ly-6_CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; Ly6 UPAR; FALSE NEG.
KW Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.
STIGNAL 1 25 By similarity.
FT CHAIN 26 105 CD59 glycoprotein.
FT PROPEP 106 131 Removed in mature form (By similarity).
FT DOMAIN 26 111 UPAR/Ly6.
FT DISULFID 28 54 By similarity.
FT DISULFID 31 41 By similarity.
FT DISUL

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FT CARBOHYD 46 46 N-linked (GlcNAc...) (Potential).
FT LIPID 105 105 GPI-anchor amidated asparagine (By
FT similarity).
SQ SEQUENCE 131 AA; 14355 MW; 47A739CBE9B4609E CRC64;

Query Match 16.9%; Score 66.5; DB 1; Length 131;
Best Local Similarity 27.9%; Pred. No. 5.3;
Matches 19; Conservative 9; Mismatches 23; Indels 17; Gaps 3;

QY 13 IKGNSSF---FLLSFFSFQNCQFCQRTTEGYAVECF-----YCLVDVAAA-- 57
Db 3 IQGGSVLFGLLLVLAFCVCHSGNSLQCYSCPLPTMESWECTASTNCTNSLDLSLIAKAGSG 62
QY 58 --FECWVF 63
Db 63 VYRCWK 70

RESULT 8
Q6MSW2 PRELIMINARY; PRT; 122 AA.
ID Q6MSW2
AC Q6MSW2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical transmembrane protein.
GN OrderedLocNames=MSC_0655;
OS Mycoplasma mycoides (subsp. mycoides SC).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=44101;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PG1;
RX PubMed=14762060; DOI=10.1101/gr.1673304;
RA Westberg J., Persson A., Holmberg A., Goemann A., Lundeberg J.,
RA Johansson K.-E., Pettersson B., Uhlen M.;
RT "The genome sequence of Mycoplasma mycoides subsp. mycoides SC type
RT strain PG1T, the causative agent of contagious bovine pleuropneumonia
RT (CBPP).";
RL Genome Res. 14:221-227(2004).
DR ENBL; BX842644; CAE77276.1; -.
DR InterPro; IPR006121; HeavyMe transp.
DR PROSITE; PS01047; HMA_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 122 AA; 14492 MW; 8A57797DCACB3107 CRC64;

Query Match 16.8%; Score 66; DB 2; Length 122;
Best Local Similarity 25.0%; Pred. No. 5.7;
Matches 14; Conservative 9; Mismatches 11; Indels 22; Gaps 2;

QY 22 LLSFFSFQNCQFCQRTTEGYAVECFYCLVDKAA-----FECWVFYSPD 67
Db 1 MLNHFNLWLCSS-----NCSPLCNKLYWFSNCLNFWSCWNFNSFN 44

RESULT 9
Q8S204 PRELIMINARY; PRT; 275 AA.
ID Q8S204
AC Q8S204;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE P0468B07.4 protein.
GN Name=P0468B07.4;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,

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RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP003260; BAB89625.1; -.
DR Gramene; Q8S204; -.
DR InterPro; IPR006209; EGF like.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
SQ SEQUENCE 275 AA; 30430 MW; 480644D61BF9B121 CRC64;

Query Match 16.8%; Score 66; DB 2; Length 275;
Best Local Similarity 33.3%; Pred. No. 12;
Matches 21; Conservative 7; Mismatches 23; Indels 12; Gaps 3;

QY 2 FVFCLILNREKIKGNSSFLLS-----FFFSFQNCQFCQRTTEGYAVECFYCL-VDK 55
Db 186 FVYSLIITAVNHGPDPSFTGVSPATVQAFSSANLNCNCFSPSL-----IFVCLATDR 239
QY 56 AAF 58
Db 240 ALF 242

RESULT 10
Q894Q5 PRELIMINARY; PRT; 304 AA.
ID Q894Q5
AC Q894Q5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Conserved protein, putative ferredoxin-type protein naph.
GN Name=naph; OrderedLocNames=CtC01480;
OS Clostridium tetani.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Massachusetts / B88;
RX MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;
RA Brueggemann H., Baumer S., Fricke W.F., Wierzer A., Liesegang H.,
RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
RA Gottschalk G.;
RT "The genome sequence of Clostridium tetani, the causative agent of
RT tetanus disease.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
DR EMBL; AE015941; AAO36037.1; -.
DR HSSP; P24184; 1KQF.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; Fer4; 2.
DR PRINTS; PR00353; 4FE4SFRDOXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
KW 4Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding.
SQ SEQUENCE 304 AA; 34263 MW; 03E4B0F10EDC52EA CRC64;

Query Match 16.5%; Score 65; DB 2; Length 304;
Best Local Similarity 27.9%; Pred. No. 17;
Matches 19; Conservative 6; Mismatches 25; Indels 18; Gaps 3;

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QY 15 GGNSSFF-----LLSFFSFQNCOCFOCR-----TTTGYAVECFYCL--VDKA 56
Db 221 GAFYSFNKISLSYDFNKDCNVCNGCRKRVCKRMDVDITKSTTHNECIRGCEIKVCP TK 280
QY 57 AFECWFY 64
Db 281 AISTFWCY 288

RESULT 11
Q91C56 PRELIMINARY; PRT; 834 AA.
AC Q91C56;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polymerase.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;

[1]
RN SEQUENCE FROM N.A.
RP Owiredu W.K., Kramvis A., Kew M.C.;
RA Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF297619; AAK97178.1; -.
DR GO; GO:0005786; C:signal recognition particle (sensu Eukaryota); IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006005; P:protein targeting; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR Pfam; PF00336; DNA_pol_viral_C; 1.
DR Pfam; PF00242; DNA_pol_viral_N; 1.
DR Pfam; PF00078; RVT_1; 2.
DR PrdDom; PD000814; DNapol_viral_C; 1.
DR RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 834 AA; 93927 MW; CSEA31F2A2230515 CRC64;

Query Match 16.4%; Score 64.5; DB 2; Length 834;
Best Local Similarity 37.1%; Pred. No. 47;
Matches 13; Conservative 6; Mismatches 7; Indels 9; Gaps 2;

QY 36 FQCHTTTGYAVECFYCLVDKAA-----PECHW 62
Db 283 FEKHSNGHVE-FHCLAPSSAGSQRGVSFPFCW 316

RESULT 12
Q6ZM73 PRELIMINARY; PRT; 1798 AA.
AC Q6ZM73;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SI:zK70P6.5 (Novel protein similar to vertebrate voltage-dependent calcium channel P/Q type alpha 1 subunit (CACNA1)) (Fragment).
DE Name=cacna1f; Synonyms=SI:zK70P6.5;
GN Name=cacna1f; Synonyms=SI:zK70P6.5;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; danio.
OX NCBI_TaxID=7955;
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RN SEQUENCE FROM N.A.
RP Beasley H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -I- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.
DR EMBL; AL331748; CAE50430.1; -.
DR ZFIN; ZDB-GENE-031104-1; cacna1f.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005891; C:voltage-gated calcium channel complex; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005245; F:voltage-gated calcium channel activity; IEA.
DR GO; GO:0006816; P:calcium ion transport; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TripL.
DR InterPro; IPR002077; Ca_channel_alpha.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005446; LVDCALphal.
DR InterPro; IPR005820; M-channel_mlg.
DR Pfam; PF00520; Ion_trans_4.
DR PRINTS; PR00167; CCHANNEL.
DR PRINTS; PR01630; LVDCALPHAL.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00214; FASP; UNKNOWN_1.
KW Calcium; Calcium channel; Calcium transport; Calcium-binding;
KW Ion transport; Ionic channel; Transmembrane; Transport;
KW Voltage-gated channel.
FT NON_TER 1
SQ SEQUENCE 1798 AA; 202714 MW; 7B9EF983772AF2DD CRC64;

Query Match 16.3%; Score 64; DB 2; Length 1798;
Best Local Similarity 36.0%; Pred. No. 1.le+02;
Matches 18; Conservative 7; Mismatches 19; Indels 6; Gaps 3;

QY 15 GGNSSFFLLSFFSFQNCOCFOCRTTTGYAVECFYCLVDKAAPECFWY 64
Db 217 GGITNFD--NEFFAM---LTVFCITMEGW-TDVLVWMDAIGFELPWVY 260

RESULT 13
O97454 PRELIMINARY; PRT; 144 AA.
AC O97454;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CG1639-PA (L(1)10Bb) (RE22390p).
GN Name=l(1)10Bb; Synonyms=lethal(1)10Bb; ORFNames=CG1639;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abell J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Kimmel B.E., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinart K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverdy T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Swirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
RT *melanogaster* euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Swirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RN SEQUENCE FROM N.A.
RP FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RN SEQUENCE FROM N.A.
RP FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RN SEQUENCE FROM N.A.
RC STRAIN=Oregon R;
RX MEDLINE=98337843; PubMed=9671597;
RA Erickson J.W., Cline T.W.;
RT "Key aspects of the primary sex determination mechanism are conserved

RT across the genus *Drosophila*.";
RL Development 125:3259-3268(1998).
RN [8]
RN SEQUENCE FROM N.A.
RP STRAIN=Oregon R;
RC STRAIN=Oregon R;
RA Erickson J.W., Salles F., Strickland S., Cline T.W.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [9]
RN SEQUENCE FROM N.A.
RP STRAIN=Berkely;
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guatin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003485; AAF48023.1; -;
DR EMBL; AF045587; AAC98483.1; -;
DR EMBL; AF046044; AAC97603.1; -;
DR EMBL; AY118623; AAM49992.1; -;
DR FlyBase; FBgn001491; l(1)10Bb.
DR GO; GO:0005634; C:nucleus; IEA.
DR InterPro; IPR010980; Cyt_c_b562.
DR InterPro; IPR01748; G10.
DR Pfam; PF01125; G10; 1.
DR PRINTS; PR00322; G10.
DR PROSITE; PS00897; G10; 1; 1.
DR PROSITE; PS00998; G10; 2; 1.
SQ SEQUENCE 144 AA; 17010 MW; 97C40F8FBC24ED3E CRC64;
Query Match 16.2%; Score 63.5; DB 2; Length 144;
Best Local Similarity 29.9%; Pred. No. 13;
Matches 20; Conservative 9; Mismatches 19; Indels 19; Gaps 4;
QY 1 MFVFCILNREKIKGN-----SSFFLLSFFFSQ-----NC-CQCFQRTTEGY 44
DB 74 LYDYCL---KEKIADNLIKWKSGYENLCRLCIQTRDTNFGTNCICRVKCKLEGR 130
QY 45 AVECFYC 51
DB 131 IVECVHC 137
RESULT 14
ID Q84TI3 PRELIMINARY; PRT; 975 AA.
AC Q84TI3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein At3g63500.
GN Name:At3g63500;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT005768; AAO64172.1; -;
DR InterPro; IPR004082; Arath130.
DR Pfam; PF07227; DUF1423; 1.
DR PRINTS; PRO1544; ARATH130DUP.
KW Hypothetical protein.

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SQ SEQUENCE 975 AA; 109142 MW; 42CFC08F431ECF62 CRC64;
Query Match 16.2%; Score 63.5; DB 2; Length 975;
Best Local Similarity 28.9%; Pred. No. 71;
Matches 22; Conservative 4; Mismatches 23; Indels 27; Gaps 5;

QY 13 IKGNSSFLLSPFFS-----FQN-----C-----CQCFCQRTTEGYAVECFY 50
Db 592 LKSGRDFLLDINSISSSHLAIEIFMNMCKNLSCRVLLPVDECDRCVSRKDGFCSCM- 650
QY 51 CLV-----DKAAFCW 62
Db 651 CLVCSNFDMASTCSW 666

RESULT 15
Q9LY65
ID Q9LY65 PRELIMINARY; PRT; 1162 AA.
AC Q9LY65;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein MAA21_130.
GN Name=MAA21_130;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W., Rudd S.,
RA Lemcke K., Mayer K.F.X., Quefier F., Salanoubat M.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL163818; CAB87803.1; -.
DR PIR; T49191; T49191.
DR InterPro; IPR004082; Arath130.
DR Pfam; PF07227; DUF1423; 1.
DR PRINTS; PR01544; ARATH130DUF.
KW Hypothetical protein.
SQ SEQUENCE 1162 AA; 130731 MW; 5B65878EC17FCC7D CRC64;
Query Match 16.2%; Score 63.5; DB 2; Length 1162;
Best Local Similarity 28.9%; Pred. No. 83;
Matches 22; Conservative 4; Mismatches 23; Indels 27; Gaps 5;

QY 13 IKGNSSFLLSPFFS-----FQN-----C-----CQCFCQRTTEGYAVECFY 50
Db 779 LKSGRDFLLDINSISSSHLAIEIFMNMCKNLSCRVLLPVDECDRCVSRKDGFCSCM- 837
QY 51 CLV-----DKAAFCW 62
Db 838 CLVCSNFDMASTCSW 853
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 50.1636 Seconds
(without alignments)
522.196 Million cell updates/sec

Title: US-10-092-934-8
Perfect score: 393
Sequence: 1 MFVFCILILNREKIKGNSSF.....FYCLVDKAAECWFWFYSDT 68

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	393	100.0	68	2 AAR63236	Aar63236 Neural th
2	393	100.0	68	2 AAR95915	Aar95915 AD 2-2 hu
3	393	100.0	68	5 AAE29149	Aae29149 Neural th
4	393	100.0	68	6 ABR63247	AbR63247 68 amino
5	393	100.0	68	6 ABU02979	Abu02979 Human neu
6	393	100.0	68	6 ABP59929	Abp59929 Human 68
7	393	100.0	68	6 AAE33196	Aae33196 Neural th
8	393	100.0	68	6 ABJ19452	Abj19452 68-mer ne
9	393	100.0	68	7 ADB37526	AdB37526 Neural th
10	393	100.0	68	7 ADL96027	Adl96027 Human neu
11	143	36.4	23	6 ABP59919	Abp59919 Human neu
12	143	36.4	23	7 ADL96065	Adl96065 Human neu
13	95	24.2	15	6 ABP59918	Abp59918 Human neu
14	95	24.2	15	7 ADL96064	Adl96064 Human neu
15	78	19.8	15	6 ABP59916	Abp59916 Human neu
16	78	19.8	15	7 ADL96062	Adl96062 Human neu
17	77	19.6	15	6 ABP59917	Abp59917 Human neu
18	77	19.6	15	7 ADL96063	Adl96063 Human neu
19	74.5	19.0	89	4 AAO02088	Aao02088 Human pol
20	67	17.0	322	4 AAU30371	Aau30371 Novel hum
21	66.5	16.9	109	7 ADC94958	Adc94958 E. faeciu
22	66.5	16.9	131	2 AAR66985	Aar66985 Squirrel
23	66.5	16.9	131	2 AAR86311	Aar86311 Ly-6 term
24	66	16.8	298	7 ADC87387	Adc87387 Human GPC
25	64.5	16.4	294	7 ADC87411	Adc87411 Human GPC

26	64.5	16.4	296	8 ADJ66555	Adj66555 Her4 prot
27	64	16.3	50	2 AAY41329	Aay41329 Human sec
28	63.5	16.2	144	4 ABB58329	Abb58329 Drosophil
29	63.5	16.2	887	8 ADN72853	Adn72853 Thale cre
30	63	16.0	30	8 ADS33534	Ads33534 CMET-HGF
31	63	16.0	128	2 AAR66986	Aar66986 Owl Monke
32	63	16.0	128	2 AAR86312	Aar86312 Ly-6 term
33	62	15.8	1824	3 AAY49431	Aay49431 Murine CA
34	62	15.8	1912	3 AAY49429	Aay49429 Human CAC
35	62	15.8	1977	3 AAY49430	Aay49430 Human CAC
36	61.5	15.6	58	2 AAY30720	Aay30720 Amino aci
37	61.5	15.6	163	3 AAB53407	Aab53407 Human col
38	61.5	15.6	301	4 AAB87732	Aab87732 Human T2R
39	61.5	15.6	301	8 ADR29064	Adr29064 Taste rec
40	61.5	15.6	302	8 ADJ84484	Adj84484 Human T2R
41	61.5	15.6	348	2 AAY05773	Aay05773 Saccharom
42	61.5	15.6	348	7 ADF39747	Adf39747 Yeast Ygl
43	61.5	15.6	449	7 ADC87301	Adc87301 Human GPC
44	61	15.5	96	4 AAM94740	Aam94740 Human rep
45	61	15.5	96	4 AAU22762	Aau22762 Human pro

ALIGNMENTS

RESULT 1
AAR63236

ID AAR63236 standard; protein; 68 AA.

XX AAR63236;

XX AC

DT 25-MAR-2003 (revised)

DT 06-JUL-1995 (first entry)

XX Neural thread protein AD2-2 T7.

XX Neural thread protein AD2-2 T7; Alzheimer's; neuroectodermal tumours;

XX Rattus rattus.

XX OS

XX Key Location/Qualifiers

FT Misc-difference 67..68

FT /note= "corresponding codons GCA CAT CAC GAC ATT TTA TAA"

XX WO9423756-A1.

PD 27-OCT-1994.

XX 20-APR-1994; 94WO-US0004321.

XX 20-APR-1993; 93US-00050559.

XX (GENO) GEN HOSPITAL CORP.

XX De La Monte SM, Wands JR;

XX WPI; 1994-341497/42.

XX N-PSDB; AAQ77872.

XX Detection of neural thread proteins - to detect sporadic and familial

XX Alzheimer's disease, neuroectodermal tumours, malignant astrocytomas and

XX glioblastomas (Eng).

XX Example 4; Fig 16a; 158pp; English.

XX AAQ77872 encodes AAR63236 the AD2-2 T7 neural thread protein (NTP). These

XX sequences were used in the development of an antibody dependent method,

XX for the detection of NTPs. This new method could be used to diagnose

XX Alzheimer's disease (differentiating between sporadic and familial),

XX neuroectodermal tumours, malignant astrocytomas and glioblastomas.

XX (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 68 AA;

Query Match 100.0%; Score 393; DB 2; Length 68;
 Best Local Similarity 100.0%; Pred. No. 5.8e-37;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFVFCILNREKIKGNSPFLLSFPPSFONCCQCFQCRRTTEGYAVECFCLVDKAAFEK 60
 DB 1 MFVFCILNREKIKGNSPFLLSFPPSFONCCQCFQCRRTTEGYAVECFCLVDKAAFEK 60
 QY 61 WWFYSPDT 68
 DB 61 WWFYSPDT 68

RESULT 2

AAR95915

ID AAR95915 standard; protein; 68 AA.

XX AC AAR95915;

XX DT 14-NOV-1996 (first entry)

XX DE AD 2-2 human neural thread protein clone (partial sequence).

XX KW Neural thread protein; NTP; diagnosis; detection; Alzheimer's disease;
 KW neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;
 KW binding fragment.

XX OS Homo sapiens.

XX PN WO9615272-A1.

XX PD 23-MAY-1996.

XX PF 14-NOV-1995; 95WO-US017111.

XX PR 14-NOV-1994; 94US-00340426.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PI De La Monte S, Wands JR;

XX DR WPI; 1996-259865/26.

XX DR N-PSDB; AAT27754.

XX PT Detection of neural thread protein in diagnosis of Alzheimer's disease -
 XX also NTP DNA and protein sequences used in gene and anti:sense therapy.

XX PS Example 4c; Fig 16A; 238pp; English.

XX CC A method for detecting the presence of neural thread protein (NTP) having
 CC a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject
 CC comprises (a) contacting a sample from a human subject that is suspected
 CC of containing the NTP with at least one molecule capable of binding to
 CC the protein; and (b) detecting any of the molecule bound to the protein.
 CC The binding molecule is selected from an antibody free of natural
 CC impurities, a monoclonal antibody or a binding fragment of either of
 CC these. The method may be used for diagnosing the presence of Alzheimer's
 CC disease, neuroectodermal tumours and a malignant astrocytoma in a human.
 CC A number of clones of neural thread protein were isolated from healthy 17
 CC -18 week old foetal human brain (HB) 2 year old temporal lobe neocortex
 CC and end stage Alzheimer's disease (AD) cerebral cortex. See AAT27753-75

SQ Sequence 68 AA;

Query Match 100.0%; Score 393; DB 2; Length 68;
 Best Local Similarity 100.0%; Pred. No. 5.8e-37;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFVFCILNREKIKGNSPFLLSFPPSFONCCQCFQCRRTTEGYAVECFCLVDKAAFEK 60
 DB 1 MFVFCILNREKIKGNSPFLLSFPPSFONCCQCFQCRRTTEGYAVECFCLVDKAAFEK 60

QY 61 WWFYSPDT 68
 DB 61 WWFYSPDT 68

RESULT 3

AAR959149

ID AAR959149 standard; protein; 68 AA.

XX AC AAR959149;

XX DT 27-JAN-2003 (first entry)

XX DE Neural thread protein (NTP) #7.

XX KW Neural thread protein; NTP; hyperplasia; hypertrophy; arteriosclerosis;
 KW haemorrhoid; gene therapy; tumour; vascular disease; atherosclerosis;
 KW inflammatory disease; nutritional deficiency disease; genetic disease;
 KW autoimmune disease; metabolic disease; traumatic disease; intoxication;
 KW infectious disease; congenital malformation; enzyme deficiency disease;
 KW amyloid disease; fibrosis disease; storage disease; radiation disease;
 KW poisoning; environmental disease; endocrine disease; protein therapy;
 KW degenerative disease; mechanical disease.

XX OS Unidentified.

XX PN WO200274323-A2.

XX PD 26-SEP-2002.

XX PF 08-MAR-2002; 2002WO-IB001959.

XX PR 08-MAR-2001; 2001US-0273957P.

XX PA (AVER/) AVERBACK P.

XX PI Averbach P;

XX DR WPI; 2002-759864/82.

XX PT Treating a condition in a patient requiring removal or destruction of
 XX cells, such as a benign or malignant tumor of a tissue or an inflammatory
 XX disease, comprises administering a neural thread protein (NTP) or a NTP
 XX gene to a mammal.

XX PS Claim 23; Fig 8; 70pp; English.

XX CC The invention relates to a method for treating a condition in a patient
 CC requiring removal or destruction of cells. The method involves
 CC administering to a mammal a neural thread protein (NTP), or administering
 CC to a tumour or other target cell a NTP gene, where the expression of the
 CC NTP gene is induced resulting in expression of the NTP protein. The
 CC method and NTP are useful for treating a condition in a patient requiring
 CC removal or destruction of cells, such as a benign or malignant tumour of
 CC a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue.
 CC preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,
 CC bacterially, or parasitically altered tissue, or a malformation of a
 CC tissue. Other conditions include a cosmetic modification to a tissue,
 CC such as removal of unwanted facial hair, warts or unwanted fatty tissue,
 CC a vascular disease, particularly atherosclerosis or arteriosclerosis,
 CC haemorrhoids, or varicose veins, an inflammatory disease, autoimmune
 CC disease, metabolic disease, hereditary/genetic disease, traumatic disease
 CC or physical injury, nutritional deficiency disease, infectious disease,
 CC congenital malformation, amyloid disease, fibrosis disease, storage
 CC disease, enzyme deficiency disease, poisoning, intoxication, degenerative
 CC disease, radiation disease, environmental disease, endocrine disease or
 CC mechanical disease. The invention is useful in protein therapy and gene
 CC therapy. The present sequence is NTP protein

SQ Sequence 68 AA;

Query Match 100.0%; Score 393; DB 5; Length 68;

Best Local Similarity 100.0%; Pred. No. 5.8e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFVFLILNREKIKGNSSFFLLSFFSFQNCOCFQCRTEGYAVECFYCLVDKAAFEK 60
DB 1 MFVFLILNREKIKGNSSFFLLSFFSFQNCOCFQCRTEGYAVECFYCLVDKAAFEK 60

QY 61 WWFYSDFT 68
DB 61 WWFYSDFT 68

RESULT 4
ABR63247
ID ABR63247 standard; protein; 68 AA.
XX AC ABR63247;
XX DT 28-AUG-2003 (first entry)
XX DE 68 amino acid neural thread protein.
XX KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour.
XX OS Unidentified.
XX WO2003008443-A2.
XX PN 30-JAN-2003.
XX PD 19-JUL-2002; 2002WO-CA001105.
XX PF 19-JUL-2001; 2001US-0306150P.
XX PR 19-JUL-2001; 2001US-0306161P.
XX PR 16-NOV-2001; 2001US-0331477P.
XX PA (NYMO-) NYMOX CORP.
XX PI Averbach PA;
XX WPI; 2003-247999/24.
XX PT Novel neural thread protein peptide, referred as cell death peptide,
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
XX PS Disclosure; Fig 8; 77pp; English.

XX The present invention relates to a neural thread protein (NTP) peptide
CC referred to as cell death peptide. Thought to be cytostatic,
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC treating a condition in a patient requiring removal or destruction of
CC cells, for treating a condition such as benign or malignant tumor,
CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for
CC a pancreatic thread protein. The peptide is conjugated, linked or bound
CC to a molecule chosen from antibody or its fragment, antibody-like binding
CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side
CC effects of surgery. The present sequence is an NTP amino acid sequence
SQ Sequence 68 AA;

Query Match 100.0%; Score 393; DB 6; Length 68;
Best Local Similarity 100.0%; Pred. No. 5.8e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFVFLILNREKIKGNSSFFLLSFFSFQNCOCFQCRTEGYAVECFYCLVDKAAFEK 60
DB 1 MFVFLILNREKIKGNSSFFLLSFFSFQNCOCFQCRTEGYAVECFYCLVDKAAFEK 60

QY 61 WWFYSDFT 68
DB 61 WWFYSDFT 68

RESULT 5
ABU02979
ID ABU02979 standard; protein; 68 AA.
XX AC ABU02979;
XX DT 20-JAN-2003 (first entry)
XX DE Human neural thread protein AD7C-NTP, protein fragment #7.
XX KW Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;
KW transplantation; grafting; chemotherapy; immunotherapy; vaccination;
KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;
KW radiation; tumour; hyperplasia; hypertrophy; overgrowth of tissue;
KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;
KW cosmetic modification; vascular disease; atherosclerosis;
KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;
KW autoimmune disease; metabolic disease; traumatic disease;
KW physical injury; nutritional deficiency disease; infectious disease;
KW amyloid disease; fibrosis disease; storage disease;
KW congenital malformation; enzyme deficiency disease; poisoning;
KW intoxication; environmental disease; radiation disease;
KW endocrine disease; degenerative disease; mechanical disease.
XX OS Homo sapiens.
XX PN WO200297030-A2.
XX PD 05-DEC-2002.
XX PF 24-MAY-2002; 2002WO-CA000759.
XX PR 25-MAY-2001; 2001US-0293156P.
XX PA (NYMO-) NYMOX CORP.
XX PI Averbach PA;
XX WPI; 2003-041406/03.
XX PT Novel peptides similar in amino acid sequence to neural thread proteins
PT (NTP), useful for treating unwanted cellular proliferations such as
PT malignant tumors and prostatic hyperplasia.
XX PS Disclosure; Fig 8; 78pp; English.

XX The invention describes an NTP-peptide (I) comprising at least one amino
CC acid sequence corresponding to part of the amino acid sequence of a
CC neural thread protein, AD7C-NTP. The invention provides a method of
CC treating a condition requiring removal or destruction of cells of a
CC mammal comprising administering to a mammal, a therapeutic amount of (I).
CC The treatment is administered to the mammal before, during or after
CC surgical excision, transplantation, grafting, chemotherapy,
CC immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,
CC laser therapy, phototherapy, gene therapy and/or radiation. The method is
CC useful for treatment of benign or malignant tumour; hyperplasia,
CC hypertrophy or overgrowth of tissue; virally, bacterially or
CC parasitically altered tissue; malformation of tissue selected from lung,
CC breast, stomach, pancreas, prostate, bladder, bone, ovary, kidney,
CC sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary
CC gland, blood, brain and its coverings, spinal cord, muscle, connective
CC tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary,
CC reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,
CC tonsils, mouth and lymph nodes and lymphoid system; tonsillary
CC hypertrophy; prostatic hyperplasia; cosmetic modification to a tissue;
CC vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;
CC varicose veins; inflammatory disease; autoimmune disease; metabolic
CC disease; hereditary/genetic disease; traumatic disease; physical injury;

CC nutritional deficiency disease; infectious disease; amyloid disease;
CC fibrosis disease; storage disease; congenital malformation; enzyme
CC deficiency disease; poisoning; intoxication; environmental disease;
CC radiation disease; endocrine disease; degenerative disease and mechanical
CC disease. This is the amino acid sequence of a human neural thread protein
CC AD7C-NTP protein fragment
XX
SQ Sequence 68 AA;

Query Match 100.0%; Score 393; DB 6; Length 68;
Best Local Similarity 100.0%; Pred. No. 5.8e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFVFCILNREIKKGNSSFFLLSPFQNCQFCQRTTEGYAVECFYCLVDKAAFEK 60
DB 1 MFVFCILNREIKKGNSSFFLLSPFQNCQFCQRTTEGYAVECFYCLVDKAAFEK 60

QY 61 WWFYSPDT 68
DB 61 WWFYSPDT 68

RESULT 6
ABP59929
ID ABP59929 standard; protein; 68 AA.

XX AC ABP59929;
XX DT 08-SEP-2003 (first entry)
XX DE Human 68 amino acid neural thread protein.
XX Human; tumour; cancer; neural thread protein; NTP; cell removal;
XX cell destruction; antipsoriatic; antimicrobial; immunosuppressive;
XX antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;
XX gene therapy.

XX OS Homo sapiens.
XX PN WO2003044053-A2.
XX PD 30-MAY-2003.

XX PF 18-NOV-2002; 2002WO-CA001757.

XX PR 16-NOV-2001; 2001US-0331477P.

XX PA (NYMO-) NYMOX CORP.

XX PI Averbach P, Gemmell J;

XX PS WPI; 2003-457592/43.

XX PT New neural thread protein (NTP), useful for preparing a composition for
PT treating or preventing a condition in a mammal requiring removal or
PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or
PT inflammatory disease.

XX PS Disclosure; Fig 6; 98pp; English.

XX CC The present invention relates to peptides derived from the human neural
CC thread protein (NTP). The peptides are useful for preparing a composition
CC for treating or preventing a condition in a mammal requiring removal or
CC destruction of cells, comprising tonsillary hypertrophy, prostatic
CC hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a
CC breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,
CC varicose veins, atherosclerosis, inflammatory, metabolic, infectious,
CC fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,
CC occlusion or blockage of an artery or of a stent placed or implanted in
CC an artery. The present sequence is an NTP protein used to produce
CC peptides of the invention

XX SQ Sequence 68 AA;

Query Match 100.0%; Score 393; DB 6; Length 68;
Best Local Similarity 100.0%; Pred. No. 5.8e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFVFCILNREIKKGNSSFFLLSPFQNCQFCQRTTEGYAVECFYCLVDKAAFEK 60
DB 1 MFVFCILNREIKKGNSSFFLLSPFQNCQFCQRTTEGYAVECFYCLVDKAAFEK 60

QY 61 WWFYSPDT 68
DB 61 WWFYSPDT 68

RESULT 7
AAE33196
ID AAE33196 standard; protein; 68 AA.

XX AC AAE33196;

XX DT 16-APR-2003 (first entry)

XX DE Neural thread protein (NTP) #7.

XX Cell death; tissue necrosis; neural thread protein; NTP; amyloidosis;
XX stroke; brain tumour; Pick's disease; Parkinson's disease; glaucoma;
XX Alzheimer's disease; gene therapy.

XX OS Unidentified.

XX PN WO200289841-A2.

XX PD 14-NOV-2002.

XX PF 06-MAY-2002; 2002WO-CA000681.

XX PR 04-MAY-2001; 2001US-0288463P.

XX PA (NYMO-) NYMOX CORP.

XX PI Averbach PA;

XX PS WPI; 2003-120506/11.

XX PT Preventing, controlling, modulating, ameliorating and/or inhibiting cell
PT death and/or tissue necrosis in live tissue containing neural thread
PT proteins (NTP). The method involves contacting the live tissue with at
PT least one antibody, fragment or derivative that recognises NTP, where the
PT antibody, fragment or derivative is present to prevent, control,
PT ameliorate and/or inhibit cell death and/or tissue necrosis caused by the
PT presence of NTP. Methods and compositions of the invention are useful for
PT preventing, modulating, controlling and/or treating disorders associated
PT with cell death and/or tissue necrosis such as stroke, brain tumour,
PT Pick's disease, Parkinson's disease, amyloidosis, glaucoma and
PT Alzheimer's disease. The invention is useful in gene therapy. The present
PT sequence is NTP protein

XX PS Disclosure; Fig 11; 60pp; English.

XX CC The invention relates to a method of preventing, and/or inhibiting cell
CC death and/or tissue necrosis in live tissue containing neural thread
CC proteins (NTP). The method involves contacting the live tissue with at
CC least one antibody, fragment or derivative that recognises NTP, where the
CC antibody, fragment or derivative is present to prevent, control,
CC ameliorate and/or inhibit cell death and/or tissue necrosis caused by the
CC presence of NTP. Methods and compositions of the invention are useful for
CC preventing, modulating, controlling and/or treating disorders associated
CC with cell death and/or tissue necrosis such as stroke, brain tumour,
CC Pick's disease, Parkinson's disease, amyloidosis, glaucoma and
CC Alzheimer's disease. The invention is useful in gene therapy. The present
CC sequence is NTP protein

XX SQ Sequence 68 AA;

Query Match 100.0%; Score 393; DB 6; Length 68;
Best Local Similarity 100.0%; Pred. No. 5.8e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFVFCILNREIKKGNSSFFLLSPFQNCQFCQRTTEGYAVECFYCLVDKAAFEK 60
DB 1 MFVFCILNREIKKGNSSFFLLSPFQNCQFCQRTTEGYAVECFYCLVDKAAFEK 60

Qy 61 WWFYSPDT 68
 Db 61 WWFYSPDT 68

RESULT 8
 ABU19452
 ID ABU19452 standard; protein; 68 AA.
 XX AC ABU19452;
 XX DT 27-MAR-2003 (first entry)
 XX DE 68-mer neural thread protein.
 XX KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
 XX KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.
 XX OS Unidentified.
 XX PN WO200292115-A2.
 XX PD 21-NOV-2002.
 XX PF 16-MAY-2002; 2002WO-CA000712.
 XX PR 16-MAY-2001; 2001US-0290971P.
 XX PA (NYMO-) NYMOX CORP.
 XX PI Averbach PA;
 XX DR WPI; 2003-129234/12.
 XX PT Preventing and/or inhibiting cell death and/or tissue necrosis in a
 PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
 PT disease, by contacting the live tissue with at least one segment of
 PT neural thread proteins (NTP).
 XX PS Disclosure; Fig 8; 60pp; English.
 XX SQ Sequence 68 AA;

Query Match 100.0%; Score 393; DB 6; Length 68;
 Best Local Similarity 100.0%; Pred. No. 5.8e-37;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRTEGVAVEFCYCLVDKAAFEK 60
 Db 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRTEGVAVEFCYCLVDKAAFEK 60

Qy 61 WWFYSPDT 68
 Db 61 WWFYSPDT 68

RESULT 9
 ADB37526
 ID ADB37526 standard; protein; 68 AA.
 XX AC ADB37526;
 XX DT 04-DEC-2003 (first entry)
 XX DE Neural thread protein #5.

XX KW Cytostatic; Antitumour; Antiprosclerotic; Dermatological;
 KW Antiatherosclerotic; Antiarteriosclerotic; Vasotropic; Antiinflammatory;
 KW Immunosuppressive; Tranquillizer; Antiemetic; Virucide; AD7c-NTP;
 KW neural thread protein; neuritic sprouting.
 XX OS Unidentified.
 XX PN WO2003008444-A2.
 XX PD 30-JAN-2003.
 XX PF 19-JUL-2002; 2002WO-CA001106.
 XX PR 19-JUL-2001; 2001US-0306150P.
 XX PR 19-JUL-2001; 2001US-0306161P.
 XX PR 16-NOV-2001; 2001US-0331477P.
 XX PA (NYMO-) NYMOX CORP.
 XX PI Averbach PA, Gemmell J;
 XX DR WPI; 2003-248000/24.
 XX PT Novel Related peptide or AD7c-neural thread peptide, useful for treating
 PT unwanted cellular proliferations, glandular hyperplasia, unwanted facial
 PT hair, warts and unwanted fatty tissue.
 XX PS Disclosure; Fig 8; 109pp; English.
 XX SQ The present invention relates to AD7c-neural thread protein (NTP) and
 CC related proteins and peptides (I; ADB37528-ADB37641). The sequences are
 CC useful for treating a condition in a patient requiring removal or
 CC destruction of cells. The condition can be selected from benign or
 CC malignant tumour of a tissue, hyperplasia, hypertrophy or overgrowth of a
 CC tissue, virally, bacterially or parasitically altered tissue, or
 CC malformation of a tissue, where the tissue is selected from lung, breast,
 CC stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney, sinus,
 CC colon, intestine, stomach, rectum, oesophagus, heart, spleen, salivary
 CC gland, blood, brain and its coverings, spinal cord and its coverings,
 CC muscle, connective tissue, adrenal, parathyroid, thyroid, uterus, testis,
 CC pituitary, reproductive organs, liver, gall bladder, eye, ear, nose,
 CC throat, tonsils, mouth, lymph nodes and lymphoid tissue. The condition is
 CC preferably tonsillary hypertrophy, prostatic hyperplasia, psoriasis,
 CC eczema, dermatosis, cosmetic modification to a tissue (skin, eye, ear,
 CC nose, throat, mouth, muscle, connective, hair or breast tissue), vascular
 CC disease (atherosclerosis or arteriosclerosis), haemorrhoids, varicose
 CC veins, inflammatory disease, autoimmune disease or physical injury,
 CC hereditary/genetic disease, traumatic disease or physical injury,
 CC nutritional deficiency disease, infectious disease, congenital malformation, enzyme
 CC fibrosis disease, storage disease, congenital malformation, enzyme
 CC deficiency disease, poisoning, intoxication, environmental disease,
 CC radiation disease, endocrine disease, degenerative disease and mechanical
 CC disease. The peptides are useful for treating unwanted cellular
 CC proliferations, glandular (e.g. prostate) hyperplasia, unwanted facial
 CC hair, warts and unwanted fatty tissue, or for preparing antibodies that
 CC recognize and/or bind to Related proteins, Related peptides or NTP
 CC peptides. The present sequence was used to illustrate the invention.
 XX SQ Sequence 68 AA;

Query Match 100.0%; Score 393; DB 7; Length 68;
 Best Local Similarity 100.0%; Pred. No. 5.8e-37;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRTEGVAVEFCYCLVDKAAFEK 60
 Db 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRTEGVAVEFCYCLVDKAAFEK 60

Qy 61 WWFYSPDT 68
 Db 61 WWFYSPDT 68

Query Match	100.0%;	Score 393;	DB 7;	Length 68;	
Best Local Similarity	100.0%;	Pred. No. 5.8e-37;			
Matches	68;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
Qy	1	MFVFCILINREKIKGGNSSFFLLSFFSFQNCQCFQCRTEGYAVECFYCLVDKAAFE	60		
Db	1	MFVFCILINREKIKGGNSSFFLLSFFSFQNCQCFQCRTEGYAVECFYCLVDKAAFE	60		
Qy	61	WWFYSDT	68		
Db	61	WWFYSDT	68		
RESULT 11					
ABP59919		ABP59919 standard; peptide; 23 AA.			
XX	AC	ABP59919;			
XX	XX				
DT	28-AUG-2003	(first entry)			
XX	XX	Human neural thread protein NTP(68) peptide #4.			
XX	XX				
KW	KW	Human; tumour; cancer; neural thread protein; NTP; cell removal;			
KW	KW	cell destruction; antipsoriatic; antimicrobial; immunosuppressive;			
KW	KW	antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;			
KW	KW	gene therapy.			
XX	XX				
OS	OS	Homo sapiens.			
XX	XX				
PN	PN	WO2003044053-A2.			
XX	XX				
PD	PD	30-MAY-2003.			
XX	XX				
PF	PF	18-NOV-2002; 2002WO-CA001757.			
XX	XX				
PR	PR	16-NOV-2001; 2001US-0331477P.			
XX	XX	(NYMO-) NYMOX CORP.			
PA	PA				
XX	XX	Averback P, Gemmell J;			
PI	PI				
XX	XX	WPI; 2003-457592/43.			
DR	DR				
XX	XX				
PT	PT	New neural thread protein (NTP), useful for preparing a composition for			
PT	PT	treating or preventing a condition in a mammal requiring removal or			
PT	PT	destruction of cells, e.g. psoriasis, eczema, atherosclerosis or			
PT	PT	inflammatory disease.			
XX	XX				
PS	PS	Claim 1; Page 39; 98pp; English.			
XX	XX				
CC	CC	The present invention relates to peptides derived from the human neural			
CC	CC	thread protein (NTP). The peptides are useful for preparing a composition			
CC	CC	for treating or preventing a condition in a mammal requiring removal or			
CC	CC	destruction of cells, comprising tonsillary hypertrophy, prostatic			
CC	CC	hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a			
CC	CC	breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,			
CC	CC	varicose veins, atherosclerosis, inflammatory, metabolic, infectious,			
CC	CC	fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,			
CC	CC	occlusion or blockage of an artery or of a stent placed or implanted in			
CC	CC	an artery. The present sequence is a peptide of the invention			
XX	XX				
SQ	SQ	Sequence 23 AA;			
Query Match	36.4%;	Score 143;	DB 6;	Length 23;	
Best Local Similarity	100.0%;	Pred. No. 4.2e-09;			
Matches	23;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;

Query Match 36.4%; Score 143; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;

DT 20-MAY-2004 (first entry)
DE Human neural thread protein, NTP68, peptide #3.
KW Human; neural thread protein; NTP122; NTP106; NTP98; NTP75;
KW NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;
KW eczema; haemorrhoid; atherosclerosis; inflammatory disease;
KW autoimmune disease; metabolic disease; hereditary disease;
KW genetic disease; traumatic disease; physical injury;
KW nutritional deficiency disease; infectious disease; amyloid disease;
KW Alzheimer's disease; storage disease; congenital malformation;
KW enzyme deficiency disease; poisoning; intoxication;
KW environmental disease; radiation disease; endocrine disease;
KW degenerative disease; mechanical disease.
OS Homo sapiens.
XX
XX US2003166569-A1.
PN
XX
XX 04-SEP-2003.
PD
XX
XX 15-NOV-2002; 2002US-00294891.
PF
XX
XX 16-NOV-2001; 2001US-0331477P.
PR
XX (AVER/) AVERBACK P.
PA (GEMM/) GEMMELL J.
PA
XX Averbach P, Gemmell J;
PI
XX WPI; 2003-898099/82.
DR
XX
XX New neural thread protein or its variants, useful for treating tumors and
XX other conditions requiring the removal or destruction of cells (e.g.
XX prostatic hyperplasia, psoriasis, eczema, hemorrhoids or
XX atherosclerosis).
XX
XX Claim 1; SEQ ID NO 43; 32pp; English.
PS
XX
XX The invention relates to a peptide, or its homologue, derivative,
XX fragment, variant or mimetic, comprising at least one neural thread
XX protein (NTP) peptide appearing as ADL96029-ADL96069, derived from
XX NTP122, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid
XX encoding an amino acid sequence corresponding to the above peptide, a
XX composition comprising one or more peptides or nucleic acids cited above
XX and a carrier, a method of treating a condition in a mammal requiring
XX removal or destruction of cells (comprising administering to the mammal
XX an amount of the peptide cited above) and a method of preventing or
XX inhibiting the stenosis, occlusion or blockage of a stent, comprising
XX coating the stent with an amount of the above peptide. The peptide
XX further comprises an amino acid in a reverse-D order based on the above
XX amino acid sequences. The composition and methods are useful in treating
XX tumours and other conditions requiring the removal or destruction of
XX cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or
XX atherosclerosis). These may also be used in treating inflammatory
XX diseases, autoimmune diseases, metabolic diseases, hereditary/genetic
XX diseases, traumatic diseases or physical injuries, nutritional deficiency
XX diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,
XX storage diseases, congenital malformation, enzyme deficiency diseases,
XX poisoning, intoxication, environmental diseases, radiation diseases,
XX endocrine diseases, degenerative diseases or mechanical diseases. The
XX present sequence is a NTP peptide of the invention.
XX
XX Sequence 15 AA;
SQ

Query Match 24.2%; Score 95; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. NO. 0.00075;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 NCCQCFQCRTEGYA 45
DB 1 NCCQCFQCRTEGYA 15

RESULT 15
ABP59916
ID ABP59916 standard; peptide; 15 AA.
XX
XX AC ABP59916;
XX
XX DT 28-AUG-2003 (first entry)
XX
XX DE Human neural thread protein NTP(68) peptide #1.
XX
XX KW Human; tumour; cancer; neural thread protein; NTP; cell removal;
KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;
KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;
KW gene therapy.
XX
XX OS Homo sapiens.
XX
XX WO2003044053-A2.
PN
XX
XX 30-MAY-2003.
PD
XX
XX 18-NOV-2002; 2002WO-CA001757.
PF
XX
XX 16-NOV-2001; 2001US-0331477P.
PR
XX (NYMO-) NYMOX CORP.
XX
XX PA Averbach P, Gemmell J;
PI
XX WPI; 2003-457592/43.
DR
XX
XX New neural thread protein (NTP), useful for preparing a composition for
XX treating or preventing a condition in a mammal requiring removal or
XX destruction of cells, e.g. psoriasis, eczema, atherosclerosis or
XX inflammatory disease.
XX
XX Claim 1; Page 38; 98pp; English.
PS
XX
XX The present invention relates to peptides derived from the human neural
XX thread protein (NTP). The peptides are useful for preparing a composition
XX for treating or preventing a condition in a mammal requiring removal or
XX destruction of cells, comprising tonsillary hypertrophy, prostatic
XX hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a
XX breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,
XX varicose veins, atherosclerosis, inflammatory, metabolic, infectious,
XX fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,
XX occlusion or blockage of an artery or of a stent placed or implanted in
XX an artery. The present sequence is a peptide of the invention
XX
XX Sequence 15 AA;
SQ

Query Match 19.8%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. NO. 0.063;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFVFCILNREKIKG 15
DB 1 MFVFCILNREKIKG 15

Search completed: October 11, 2005, 07:11:14
Job time : 53.3636 secs

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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:16 ; Search time 114 Seconds

(without alignments)
248.149 Million cell updates/sec

Title: US-10-092-934-8

Perfect score: 393

Sequence: 1 MFVFCILNREKIKGGNSF.....FYCLVDKAAPECWWFYSFDT 68

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	393	100.0	68	14	US-10-138-516-7
2	393	100.0	68	14	US-10-146-130-9
3	393	100.0	68	14	US-10-092-934-8
4	393	100.0	68	14	US-10-153-334-8
5	393	100.0	68	14	US-10-198-069-8
6	393	100.0	68	14	US-10-198-070-8
7	393	100.0	68	14	US-10-294-891-6
8	393	100.0	68	17	US-10-920-313-6
9	143	36.4	23	14	US-10-294-891-44
10	143	36.4	23	17	US-10-920-313-44
11	95	24.2	15	14	US-10-294-891-43
					Sequence 7, Appli
					Sequence 9, Appli
					Sequence 8, Appli
					Sequence 8, Appli
					Sequence 8, Appli
					Sequence 8, Appli
					Sequence 6, Appli
					Sequence 6, Appli
					Sequence 4, Appli
					Sequence 44, Appli
					Sequence 43, Appli

12	95	24.2	15	17	US-10-920-313-43	Sequence 43, Appli
13	78	19.8	15	14	US-10-294-891-41	Sequence 41, Appli
14	78	19.8	15	17	US-10-920-313-41	Sequence 41, Appli
15	77	19.6	15	14	US-10-294-891-42	Sequence 42, Appli
16	77	19.6	15	17	US-10-920-313-42	Sequence 42, Appli
17	68	17.3	172	15	US-10-424-599-158515	Sequence 158515,
18	67.5	17.2	1116	16	US-10-437-963-162468	Sequence 162468,
19	66	16.8	298	14	US-10-017-161-2194	Sequence 2194, Ap
20	66	16.8	298	15	US-10-292-798-1840	Sequence 1840, Ap
21	65	16.5	97	15	US-10-424-599-210426	Sequence 210426,
22	64.5	16.4	294	14	US-10-017-161-2218	Sequence 2218, Ap
23	64.5	16.4	294	15	US-10-292-798-1864	Sequence 1864, Ap
24	64	16.3	49	15	US-10-653-595-132	Sequence 132, App
25	64	16.3	50	10	US-09-397-945-132	Sequence 132, App
26	64	16.3	103	15	US-10-424-599-220535	Sequence 220535,
27	63.5	16.2	144	20	US-11-097-143-1779	Sequence 1779, App
28	63	16.0	30	18	US-10-792-582-187	Sequence 187, App
29	63	16.0	144	16	US-10-425-115-297883	Sequence 297883,
30	62	15.8	53	15	US-10-425-115-297729	Sequence 177729,
31	62	15.8	102	16	US-10-425-115-232872	Sequence 232872,
32	62	15.8	1966	18	US-10-828-868-5	Sequence 5, Appli
33	62	15.8	1966	18	US-10-828-868-6	Sequence 6, Appli
34	62	15.8	1977	18	US-10-828-868-7	Sequence 7, Appli
35	61.5	15.6	57	15	US-10-632-983-67	Sequence 121, App
36	61.5	15.6	84	15	US-10-632-983-121	Sequence 107755,
37	61.5	15.6	134	16	US-10-437-963-107755	Sequence 18, Appli
38	61.5	15.6	162	9	US-09-798-789-18	Sequence 428, App
39	61.5	15.6	162	14	US-10-218-102-428	Sequence 947, App
40	61.5	15.6	163	9	US-09-925-299-947	Sequence 947, App
41	61.5	15.6	163	10	US-09-925-299-947	Sequence 3, Appli
42	61.5	15.6	301	16	US-10-770-127-3	Sequence 3, Appli
43	61.5	15.6	302	9	US-09-393-634-37	Sequence 37, Appli
44	61.5	15.6	302	10	US-09-510-332-3	Sequence 37, Appli
45	61.5	15.6	302	14	US-10-383-982-37	Sequence 37, Appli

ALIGNMENTS

RESULT 1

US-10-138-516-7
; Sequence 7, Application US/10138516
; Publication No. US20030003445A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING ANTIBODIES TO
; TITLE OF INVENTION: NEURAL THREAD PROTEINS
; FILE REFERENCE: 59003.000004
; CURRENT APPLICATION NUMBER: US/10138,516
; CURRENT FILING DATE: 2002-07-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-516-7

Query Match 100.0%; Score 393; DB 14; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.3e-38;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MFVFCILNREKIKGGNSFFLLSFFFSFONCCOCFQRTTEGVAVCFYCLVDKAAPEC	60
Db	1	MFVFCILNREKIKGGNSFFLLSFFFSFONCCOCFQRTTEGVAVCFYCLVDKAAPEC	60
	61	WWFYSFDT	68
	61	WWFYSFDT	68

RESULT 2

US-10-146-130-9


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US-10-198-070-8
; Sequence 8, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Unknown NTP
; OTHER INFORMATION: peptide
US-10-198-070-8

Query Match      100.0%; Score 393; DB 14; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.3e-38;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRITTEGYAVECFYCLVDKAAPEC 60
Db 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRITTEGYAVECFYCLVDKAAPEC 60

Qy 61 WWFYSFDT 68
Db 61 WWFYSFDT 68

RESULT 7
US-10-294-891-6
; Sequence 6, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-6

Query Match      100.0%; Score 393; DB 14; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.3e-38;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRITTEGYAVECFYCLVDKAAPEC 60
Db 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRITTEGYAVECFYCLVDKAAPEC 60

Qy 61 WWFYSFDT 68
Db 61 WWFYSFDT 68

US-10-198-070-8
; Sequence 8, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Unknown NTP
; OTHER INFORMATION: peptide
US-10-198-070-8

Query Match      100.0%; Score 393; DB 14; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.3e-38;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRITTEGYAVECFYCLVDKAAPEC 60
Db 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRITTEGYAVECFYCLVDKAAPEC 60

Qy 61 WWFYSFDT 68
Db 61 WWFYSFDT 68

RESULT 7
US-10-294-891-6
; Sequence 6, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-6

Query Match      100.0%; Score 393; DB 14; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.3e-38;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRITTEGYAVECFYCLVDKAAPEC 60
Db 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRITTEGYAVECFYCLVDKAAPEC 60

Qy 61 WWFYSFDT 68
Db 61 WWFYSFDT 68
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Db 61 WWFYSFDT 68

RESULT 8
US-10-920-313-6
; Sequence 6, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-6

Query Match      100.0%; Score 393; DB 17; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.3e-38;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRITTEGYAVECFYCLVDKAAPEC 60
Db 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRITTEGYAVECFYCLVDKAAPEC 60

Qy 61 WWFYSFDT 68
Db 61 WWFYSFDT 68

RESULT 9
US-10-294-891-44
; Sequence 44, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-44

Query Match      36.4%; Score 143; DB 14; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 VECFYCLVDKAAAECEWFWYSFDT 68
Db 1 VECFYCLVDKAAAECEWFWYSFDT 23

RESULT 10
US-10-920-313-44
; Sequence 44, Application US/10920313
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; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-44

Query Match          36.4%; Score 143; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 VECFYCLVDKAAECWFWYSFDT 68
Db 1 VECFYCLVDKAAECWFWYSFDT 23

RESULT 11
US-10-294-891-43
; Sequence 43, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-43

Query Match          24.2%; Score 95; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 NCCQCFQCRRTTEGYA 45
Db 1 NCCQCFQCRRTTEGYA 15

RESULT 12
US-10-920-313-43
; Sequence 43, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
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; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-43

Query Match          24.2%; Score 95; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 NCCQCFQCRRTTEGYA 45
Db 1 NCCQCFQCRRTTEGYA 15

RESULT 13
US-10-294-891-41
; Sequence 41, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-41

Query Match          19.8%; Score 78; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFVFCLILNREKIKG 15
Db 1 MFVFCLILNREKIKG 15

RESULT 14
US-10-920-313-41
; Sequence 41, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-41

Query Match          19.8%; Score 78; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MFVFCILINREKIG 15
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Db 1 MFVFCILINREKIG 15

RESULT 15
US-10-294-891-42
; Sequence 42, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-42

Query Match 19.6%; Score 77; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 GNSSFLLSPFFSFQ 30
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Db 1 GNSSFLLSPFFSFQ 15

Search completed: October 11, 2005, 07:39:47
Job time : 115 secs

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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:19 ; Search time 15.5455 Seconds
(without alignments)
326.535 Million cell updates/sec

Title: US-10-092-934-8
Perfect score: 393
Sequence: 1 MFVFCILNREKIKGNSSP.....FYCLVDKAAPECFWYFSDT 68

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	393	100.0	68	2	US-08-454-557C-36
2	393	100.0	68	2	US-08-340-426D-36
3	393	100.0	68	2	US-08-450-673C-36
4	393	100.0	68	5	PCT-US95-17111A-36
5	234	59.5	75	4	US-09-621-976-5918
6	207	52.7	75	4	US-09-621-976-5886
7	66.5	16.9	109	4	US-09-107-532A-4585
8	64	16.3	119	4	US-09-270-767-37122
9	64	16.3	119	4	US-09-270-767-52339
10	64	16.3	188	4	US-09-270-767-40814
11	64	16.3	188	4	US-09-270-767-56030
12	62	15.8	1912	4	US-09-495-714C-2
13	62	15.8	1977	4	US-09-495-714C-4
14	62	15.8	1985	4	US-09-495-714C-6
15	61.5	15.6	58	4	US-09-716-129-67
16	61.5	15.6	84	4	US-09-716-129-121
17	61.5	15.6	302	4	US-09-393-634-37
18	61.5	15.6	348	4	US-09-415-277C-14
19	60.5	15.4	5179	4	US-09-538-092-1258
20	59.5	15.1	845	4	US-08-591-502B-57
21	59	15.0	404	2	US-08-070-301-15
22	58.5	14.9	105	3	US-08-858-207A-551
23	58	14.8	115	4	US-09-513-999C-7845
24	58	14.8	115	4	US-09-513-999C-7846
25	58	14.8	115	4	US-09-513-999C-7847
26	58	14.8	128	6	5179198-1
27	58	14.8	128	6	5521296-1

28	58	14.8	128	6	5179198-1	Patent No. 5179198
29	58	14.8	128	6	5521296-1	Patent No. 5521296
30	58	14.8	135	4	US-09-949-016-9460	Sequence 9460, Ap
31	58	14.8	270	4	US-09-134-000C-5367	Sequence 5367, Ap
32	58	14.8	437	4	US-09-543-681A-7455	Sequence 7455, Ap
33	56	14.2	123	3	US-09-134-001C-5115	Sequence 5115, Ap
34	56	14.2	141	4	US-09-270-767-36649	Sequence 36649, A
35	56	14.2	141	4	US-09-270-767-51866	Sequence 51866, A
36	56	14.2	282	4	US-09-270-767-40352	Sequence 40352, A
37	56	14.2	282	4	US-09-270-767-55568	Sequence 55568, A
38	56	14.2	301	4	US-09-270-767-41523	Sequence 41523, A
39	56	14.2	2161	1	US-07-745-206A-2	Sequence 2, Appli
40	56	14.2	2161	1	US-08-455-543A-49	Sequence 49, Appl
41	56	14.2	2161	2	US-08-223-305C-49	Sequence 49, Appl
42	56	14.2	2161	2	US-08-311-363-2	Sequence 2, Appli
43	55.5	14.1	258	4	US-09-252-991A-19825	Sequence 19825, A
44	55.5	14.1	424	4	US-09-270-767-37179	Sequence 37179, A
45	55.5	14.1	424	4	US-09-270-767-52396	Sequence 52396, A

ALIGNMENTS

RESULT 1
US-08-454-557C-36
; Sequence 36, Application US/08454557C
; Patent No. 5830670
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,557C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

US-08-454-557C-36
Query Match 100.0%; Score 393; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.6e-41;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MFVFCILNREKIKGNSSFFLLSFFSFQNCOCFOCRITTEGYAVECFCLVDKAAPEC 60
Db	1	MFVFCILNREKIKGNSSFFLLSFFSFQNCOCFOCRITTEGYAVECFCLVDKAAPEC 60
Qy	61	WWFYSFDT 68

```
Db 61 WWFYSFDT 68

RESULT 2
US-08-340-426D-36
; Sequence 36, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,426D
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 36:
; LENGTH: 68 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-340-426D-36

Query Match 100.0%; Score 393; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.6e-41;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFVFCILNREKIKGNSFFLLSFFSFQNCQCFQCRTEGYAVECFYCLVDKAAFE 60
Db 1 MFVFCILNREKIKGNSFFLLSFFSFQNCQCFQCRTEGYAVECFYCLVDKAAFE 60

QY 61 WWFYSFDT 68
Db 61 WWFYSFDT 68

RESULT 4
PCT-US95-17111A-36
; Sequence 36, Application PC/TUS9517111A
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
; TITLE OF INVENTION: Detection of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17111A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,426
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; INFORMATION FOR SEQ ID NO: 36:
; TYPE: amino acid
; LENGTH: 68 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-450-673C-36

Query Match 100.0%; Score 393; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.6e-41;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFVFCILNREKIKGNSFFLLSFFSFQNCQCFQCRTEGYAVECFYCLVDKAAFE 60
Db 1 MFVFCILNREKIKGNSFFLLSFFSFQNCQCFQCRTEGYAVECFYCLVDKAAFE 60

QY 61 WWFYSFDT 68
Db 61 WWFYSFDT 68

RESULT 3
US-08-450-673C-36
; Sequence 36, Application US/08450673C
; Patent No. 5948888
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
```



```
;
; LENGTH: 68 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US95-17111A-36

Query Match      100.0%; Score 393; DB 5; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.6e-41;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRTEGYAVCEFCYCLVDKAAPEC 60
   |||||
Db 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRTEGYAVCEFCYCLVDKAAPEC 60
   |||||

Qy 61 WWFYSDFT 68
   |||||
Db 61 WWFYSDFT 68

RESULT 5
US-09-621-976-5918
; Sequence 5918, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5918
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -37..-1
; NAME/KEY: UNSURE
; LOCATION: 28
; OTHER INFORMATION: Xaa = Pro,Ser
US-09-621-976-5918

Query Match      59.5%; Score 234; DB 4; Length 75;
Best Local Similarity 64.7%; Pred. No. 1.1e-21;
Matches 44; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRTEGYAVCEFCYCLVDKAAPEC 60
   |||||
Db 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRTEGYAVCEFCYCLVDKAAPEC 60
   |||||

Qy 61 WWFYSDFT 68
   |||||
Db 61 WWFYSDFT 68

RESULT 6
US-09-621-976-5886
; Sequence 5886, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5886
; LENGTH: 75
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -37..-1
; NAME/KEY: UNSURE
; LOCATION: 35
; OTHER INFORMATION: Xaa = *,Tyr
; NAME/KEY: UNSURE
; LOCATION: 31
; OTHER INFORMATION: Xaa = Ala,Pro,Ser,Thr
; NAME/KEY: UNSURE
; LOCATION: 27
; OTHER INFORMATION: Xaa = Asn,Tyr
; NAME/KEY: UNSURE
; LOCATION: 25
; OTHER INFORMATION: Xaa = Gly,Trp
; NAME/KEY: UNSURE
; LOCATION: 10
; OTHER INFORMATION: Xaa = Lys,Arg
US-09-621-976-5886

Query Match      52.7%; Score 207; DB 4; Length 75;
Best Local Similarity 61.2%; Pred. No. 2.3e-18;
Matches 41; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRTEGYAVCEFCYCLVDKAAPEC 60
   |||||
Db 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRTEGYAVCEFCYCLVDKAAPEC 60
   |||||

Qy 61 WWFYSDFT 67
   |||||
Db 61 WWFYSDFT 67

RESULT 7
US-107-532A-4585
; Sequence 4585, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107.532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4585:
; SEQUENCE CHARACTERISTICS:
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```

; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...109
; SEQUENCE DESCRIPTION: SEQ ID NO: 4585:
US-09-107-532A-4585

Query Match      16.9%; Score 66.5; DB 4; Length 109;
Best Local Similarity 33.3%; Pred. No. 0.7;
Matches 17; Conservative 7; Mismatches 20; Indels 7; Gaps 3;

QY 19 SFPELLSFFSFQ-NC--CQCFQCTTTGGYAVECFYCLVDKKAAPFCWFWYF 66
Db 26 SCFLCYFHYSSPYCRFCSCFLCYFHYSSPYCFRC----SCFLCYFHCYS 72

RESULT 8
US-09-270-767-37122
; Sequence 37122, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37122
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-37122

Query Match      16.3%; Score 64; DB 4; Length 119;
Best Local Similarity 29.2%; Pred. No. 1.6;
Matches 21; Conservative 10; Mismatches 19; Indels 22; Gaps 5;

QY 2 FVFCILNREIKGNSFFLLSFFSFQNCQCQCQRTTGGYA--VECFYCL---VDKA 56
Db 17 FFPCLV-----FGWTFWPGF---CFCFFSRLFFSLAGVACPFPSAGRRRSR 61

QY 57 AFEC--WFWYF 66
Db 62 SLFCFIWFFFSF 73

RESULT 9
US-09-270-767-52339
; Sequence 52339, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52339
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-52339

Query Match      16.3%; Score 64; DB 4; Length 119;
Best Local Similarity 22.2%; Pred. No. 1.6;

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```

; GENERAL INFORMATION:
; APPLICANT: University Technologies International Inc.
; TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) 1F-SUBUNIT GENE
; FILE REFERENCE: 45499.4 (formerly 45074.6)
; CURRENT APPLICATION NUMBER: US/09/495,714C
; CURRENT FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1912
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-495-714C-2

Query Match          15.8%; Score 62; DB 4; Length 1912;
Best Local Similarity 34.0%; Pred. No. 52;
Matches 17; Conservative 8; Mismatches 19; Indels 6; Gaps 3;

QY 15 GGNSSFFLLSFFSFQNCQCFCQRTTEGYAVECFYCLVDKAAFECEWFWY 64
Db 243 GGIITFD--NFFFM---LTVFQCVTMEGW-TDVLVYMQDAMGYELPFWY 286

RESULT 13
US-09-495-714C-4
; Sequence 4, Application US/09495714C
; Patent No. 6670465
; GENERAL INFORMATION:
; APPLICANT: University Technologies International Inc.
; TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) 1F-SUBUNIT GENE
; FILE REFERENCE: 45499.4 (formerly 45074.6)
; CURRENT APPLICATION NUMBER: US/09/495,714C
; CURRENT FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-495-714C-4

Query Match          15.8%; Score 62; DB 4; Length 1977;
Best Local Similarity 34.0%; Pred. No. 54;
Matches 17; Conservative 8; Mismatches 19; Indels 6; Gaps 3;

QY 15 GGNSSFFLLSFFSFQNCQCFCQRTTEGYAVECFYCLVDKAAFECEWFWY 64
Db 308 GGIITFD--NFFFM---LTVFQCVTMEGW-TDVLVYMQDAMGYELPFWY 351

RESULT 14
US-09-495-714C-6
; Sequence 6, Application US/09495714C
; Patent No. 6670465
; GENERAL INFORMATION:
; APPLICANT: University Technologies International Inc.
; TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) 1F-SUBUNIT GENE
; FILE REFERENCE: 45499.4 (formerly 45074.6)
; CURRENT APPLICATION NUMBER: US/09/495,714C
; CURRENT FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1985
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-495-714C-6

Query Match          15.8%; Score 62; DB 4; Length 1985;
Best Local Similarity 34.0%; Pred. No. 54;
Matches 17; Conservative 8; Mismatches 19; Indels 6; Gaps 3;

QY 15 GGNSSFFLLSFFSFQNCQCFCQRTTEGYAVECFYCLVDKAAFECEWFWY 64
```

```

Db 308 GGIITFD--NFFFM---LTVFQCVTMEGW-TDVLVYMQDAMGYELPFWY 351

RESULT 15
US-09-716-129-67
; Sequence 67, Application US/09716129
; Patent No. 6632920
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 36 Human Secreted Proteins
; FILE REFERENCE: P2025P1
; CURRENT APPLICATION NUMBER: US/09/716,129
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/076,053
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,057
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,052
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,054
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,051
; PRIOR FILING DATE: 1998-02-26
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: Xaa equals stop translation
US-09-716-129-67

Query Match          15.6%; Score 61.5; DB 4; Length 58;
Best Local Similarity 35.9%; Pred. No. 1.5;
Matches 14; Conservative 5; Mismatches 17; Indels 3; Gaps 1;

QY 19 SFFLLSFFSFQNCQCFCQRTTEGYAVECFYCLVDKAA 57
Db 19 SLFLQWLFFGLQCCSSFLCRKNES---QCFTRLKERSA 54

Search completed: October 11, 2005, 07:42:52
Job time : 16.5455 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 9.45989 Seconds
(without alignments)
620.432 Million cell updates/sec

Title: US-10-092-934-9
Perfect score: 326
Sequence: 1 MEHTVAQGVPOHDLGSLQ.....NMNTALKRNRYTPETGRKS 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR.79.*
2: PIR.2.*
3: PIR.3.*
4: PIR.4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121.5	37.3	613	4 C40201	artifact-warning s
2	118	36.2	46	2 I54375	gene NF2 protein -
3	117.5	36.0	627	4 A40201	artifact-warning s
4	117	35.9	39	2 I54374	gene NF2 protein -
5	112	34.4	53	2 A42442	integrin beta-1 ch
6	97.5	29.9	673	4 F40201	artifact-warning s
7	76.5	23.5	597	4 E40201	artifact-warning s
8	72	22.1	440	2 A26359	decay-accelerating
9	67	20.6	331	2 A54295	interferon alpha/b
10	67	20.6	331	2 S59501	interferon recepto
11	63	19.3	522	2 T08711	gamma-adaptin homo
12	60.5	18.6	660	2 H87325	hypothetical prote
13	60.5	18.6	814	2 A35206	glycosyl transfera
14	59.5	18.3	516	2 T32489	hypothetical prote
15	59	18.1	1239	2 A45648	DNA topoisomerase
16	57	17.5	446	2 E71057	probable thiamin b
17	57	17.5	747	2 T40728	hypothetical prote
18	56.5	17.3	245	2 S48363	hypothetical prote
19	56.5	17.3	718	2 H75485	hypothetical prote
20	56.5	17.3	1615	2 J06510	ras-responsive ele
21	56	17.2	691	2 S48390	hypothetical prote
22	55.5	17.0	427	2 T29872	hypothetical prote
23	55.5	17.0	747	2 T39879	hypothetical prote
24	55.5	17.0	947	2 G86420	probable receptor-
25	55.5	17.0	1196	2 S65245	translation elonga
26	55	16.9	189	2 F89753	protein FltC7.5 li
27	55	16.9	246	2 A70310	conserved hypothet
28	55	16.9	380	2 H69427	probable 2,3-bisph
29	55	16.9	394	2 H75372	conserved hypothet

30 55 16.9 454 2 T16429
31 55 16.9 508 2 T00753
32 55 16.9 1113 2 S73327
33 54.5 16.7 197 2 T40144
34 54.5 16.7 711 2 C83922
35 54 16.6 314 2 G64940
36 54 16.6 314 2 H85790
37 54 16.6 314 2 D90942
38 54 16.6 682 2 T15092
39 54 16.6 929 2 JH0262
40 53.5 16.4 210 2 G84499
41 53.5 16.4 261 2 C72128
42 53.5 16.4 261 2 F86494
43 53.5 16.4 329 2 T17033
44 53.5 16.4 354 2 S75877
45 53.5 16.4 361 2 G83981

ALIGNMENTS

RESULT 1

C40201
artifact-warning sequence (translated ALU class C) - human

C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000

C:Accession: C40201
R:Claverie, J.M.

personal communication, 1992

A:Reference number: A40201

A:Accession: C40201

A:Molecule type: DNA

A:Residues: 1-613 <CUA>

R:Claverie, J.M.

Genomics 12, 838-841, 1992

A:Title: Identifying coding exons by similarity search: Alu-derived and other potential

A:Reference number: A40200; MUID:92241891; PMID:1572661

A:Contents: annotation

C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames of

in-frame stop codons are shown as 'X'.

C:Comment: Any significant similarity of a predicted protein sequence to a portion of the

Query Match 37.3%; Score 121.5; DB 4; Length 613;

Best Local Similarity 47.5%; Pred. No. 1.9e-07;

Matches 28; Conservative 5; Mismatches 21; Indels 5; Gaps 1;

Oy 2 EPHTVAQGVPOHDLGSLQSLPRKPFSCILIPKIDYRNMTA----LIKRNRYTP 55

Db 318 EHSVTAQGVQWRDLGSLQAPPFGMPFSCLSLRTWDRPHHAQLIFCFSRNGVLP 376

RESULT 2

154375

gene NF2 protein - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 16-Aug-2004

C:Accession: I54375

R:Arakawa, H.; Hayashi, N.; Nagase, H.; Ogawa, M.; Nakamura, Y.

Hum. Mol. Genet. 3, 565-568, 1994

A:Title: Alternative splicing of the NF2 gene and its mutation analysis of breast and co

A:Reference number: I54375; MUID:94348501; PMID:8069299

A:Accession: I54375

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-46 <RES>

A:Cross-references: UNIPROT:Q16230; GB:S73853; NID:g688372; PIDN:AAB31736.1; PID:g688373

C:Genetics:

A:Gene: GDB:NF2

A:Cross-references: GDB:I20232; OMIM:101000

A:Map position: 22q12.2-22q12.2

C:Superfamily: laminin-type EGF-like homology

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 36.6163 Seconds
(without alignments)
853.085 Million cell updates/sec

Title: US-10-092-934-9

Perfect score: 326

Sequence: 1 MEGHTVAQAGVPOHDLGSLQ.....NMNTALIKRNYTPTGRKS 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155	47.5	128	2 Q8N862	Q8N862 homo sapien
2	141.5	43.4	165	2 Q6ZS53	Q6ZS53 homo sapien
3	141.5	43.4	165	2 Q6ZT71	Q6ZT71 homo sapien
4	140	42.9	434	2 Q8N213	Q8N213 homo sapien
5	140	42.9	440	2 Q8N273	Q8N273 homo sapien
6	136	41.7	142	2 Q6ZWD5	Q6ZWD5 homo sapien
7	135	41.4	83	2 Q96ID7	Q96ID7 homo sapien
8	135	41.4	151	2 Q6NS37	Q6NS37 homo sapien
9	134.5	41.3	591	1 ALU8_HUMAN	P39195 homo sapien
10	134	41.1	122	2 Q6ZNY9	Q6ZNY9 homo sapien
11	133.5	41.0	72	2 Q8TB48	Q8TB48 homo sapien
12	132.5	40.6	132	2 Q6ZNG3	Q6ZNG3 homo sapien
13	132	40.5	66	2 Q96HL9	Q96HL9 homo sapien
14	131	40.2	123	2 Q6ZV58	Q6ZV58 homo sapien
15	131	40.2	151	2 Q8HA67	Q8HA67 homo sapien
16	130.5	40.0	375	2 Q6O448	Q6O448 homo sapien
17	130	39.9	73	2 Q96AN9	Q96AN9 homo sapien
18	130	39.9	151	2 Q8N287	Q8N287 homo sapien
19	129.5	39.7	593	1 ALU7_HUMAN	P39194 homo sapien
20	129	39.6	131	2 Q8ZTD3	Q8ZTD3 homo sapien
21	128	39.3	123	2 Q6ZMQ3	Q6ZMQ3 homo sapien
22	128	39.3	193	2 Q6ZVX8	Q6ZVX8 homo sapien
23	128	39.3	630	2 Q8N7U6	Q8N7U6 homo sapien
24	127	39.0	118	2 Q9P195	Q9P195 homo sapien
25	127	39.0	659	2 Q7OAC3	Q7OAC3 homo sapien
26	127	39.0	726	2 Q7O8E2	Q7O8E2 homo sapien
27	125	38.3	788	2 Q6ZMV3	Q6ZMV3 homo sapien
28	124.5	38.2	170	2 Q6ZV14	Q6ZV14 homo sapien
29	124	38.0	102	2 Q9P147	Q9P147 homo sapien
30	124	38.0	132	2 Q6ZVC2	Q6ZVC2 homo sapien
31	123.5	37.9	587	1 ALU2_HUMAN	P39189 homo sapien

32	123.5	37.9	587	1 ALU3_HUMAN	P39190 homo sapien
33	123.5	37.9	593	1 ALU6_HUMAN	P39193 homo sapien
34	123	37.7	506	2 Q9H6L7	Q9H6L7 homo sapien
35	122.5	37.6	157	2 Q8N845	Q8N845 homo sapien
36	122.5	37.6	208	2 Q9NWI4	Q9NWI4 homo sapien
37	122	37.4	122	2 Q6ZVH4	Q6ZVH4 homo sapien
38	122	37.4	158	2 Q8NAL9	Q8NAL9 homo sapien
39	122	37.4	602	2 Q6ZNH6	Q6ZNH6 homo sapien
40	121.5	37.3	585	1 ALU5_HUMAN	P39192 homo sapien
41	121	37.1	122	2 Q9BGW3	Q9BGW3 macaca fasc
42	121	37.1	164	2 Q8UQD6	Q8UQD6 homo sapien
43	120	36.8	138	2 Q8N874	Q8N874 homo sapien
44	120	36.8	198	2 Q6ZS18	Q6ZS18 homo sapien
45	120	36.8	840	2 Q6NY19	Q6NY19 homo sapien

ALIGNMENTS

RESULT 1

Q8N862	Q8N862	PRELIMINARY;	PRT;	128 AA.
AC	Q8N862:			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DE	Hypothetical protein FLJ39947.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RX	PubMed=14702039; DOI=10.1038/ngi1285;			
RA	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,			
RA	Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,			
RA	Sekine M., Oabayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,			
RA	Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,			
RA	Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,			
RA	Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,			
RA	Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,			
RA	Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,			
RA	Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,			
RA	Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,			
RA	Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,			
RA	Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,			
RA	Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,			
RA	Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,			
RA	Yoshihara Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,			
RA	Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,			
RA	Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,			
RA	Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,			
RA	Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,			
RA	Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,			
RA	Ono T., Yamada K., Fujii Y., Ozaki K., Hiraoka M., Ohmori Y.,			
RA	Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,			
RA	Okitani R., Kawakami T., Noguchi S., Itoh T., Shigetani K., Senba T.,			
RA	Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,			
RA	Togashi T., Oyano M., Hata H., Watanabe M., Komatsu T.,			
RA	Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,			
RA	Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,			
RA	Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,			
RT	"Complete sequencing and characterization of 21,243 full-length human			
RL	CDNAs."			
RL	Nat. Genet. 36:40-45(2004) .			
DR	EMBL: AK097266; BAC04988.1; -.			
SQ	SEQUENCE 128 AA; 13990 MW; CEF28D6A02AE709F CRC64;			

Query Match 47.5%; Score 155; DB 2; Length 128;
Best Local Similarity 71.4%; Pred. No. 1.1e-11;
Matches 30; Conservative 3; Mismatches 9; Indels 0; Gaps 0;


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QY 1 MEPHTVAQGVPOHDLGSLQSLPRPKRFSCLILPKIWDYR 41
Db 93 MESHSVTQAGQWHDLSLQALPGFMPFSCLSLPSWNYR 133

RESULT 9
ALU8 HUMAN
ID ALU8_HUMAN STANDARD; PRT; 591 AA.
AC P39195;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alu subfamily SX sequence contamination warning entry.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95021759; PubMed=7935834; DOI=10.1038/371752a0;
RA Claverie J.-M., Makalowski W.;
RT "Alu alert.";
RL Nature 371:752-752(1994).
RN [2]
RP CONCEPT.
RX MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.;
RT "Identifying coding exons by similarity search: alu-derived and other
potentially misleading protein sequences.";
RL Genomics 12:838-841(1992).
RN [3]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA Quentin Y.;
RT "The Alu family developed through successive waves of fixation closely
connected with primate lineage history.";
RL J. Mol. Evol. 27:194-202(1988).
RN [4]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J., Milosavljevic A.;
RT "Reconstruction and analysis of human Alu genes.";
RL J. Mol. Evol. 32:105-121(1991).
CC -1- MISCELLANEOUS: Various analyses indicate that Alu repeats fall
into 8 subfamilies (Ref.3 and Ref.4). Therefore, 8 Alu warning
consensus sequences have been constituted that contain all six
frames conceptual translations of each of these classes of Alu
repeats
CC -1- MISCELLANEOUS: Isolated 'X' indicates the presence of a stop
codon, 'XXX' is used to separate the various translation phases.
CC -1- CAUTION: This Alu entry is provided in order to avoid the further
pollution of protein sequence databases with Alu-derived amino
acid sequences
CC -1- CAUTION: Alu repetitive sequences are interspersed in human and
primate genomes with an average spacing of 4 kb. Some of them are
actively transcribed by pol III. Normal transcripts may contain
Alu-derived sequences in 5' or 3' untranslated regions. However,
cDNA libraries also contain partial and/or rearranged cDNAs
ligated with Alu-derived sequence in any orientation. Although Alu
elements (especially situated on the complementary strand) have a
great potential to create additional/alternative exons,
consideration should be given to the possibility that the presence
of an Alu in an open reading frame may have resulted from a
cloning artifact or may be due to misinterpretation of sequencing
data. This point has been overlooked on several occasions, with
the consequence of erroneous Alu-derived amino acid sequences
being reported.
CC -1- CAUTION: Any significant similarity of a putative protein sequence
with an Alu-translated entry must be taken as a warning that a
part of Alu repeat may have been artifactually included in the
coding nucleotide sequence.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U14574; -; NOT ANNOTATED_CDS.
KW Hypothetical protein.
FT DOMAIN 1 96 Frame-1.
FT DOMAIN 100 195 Frame-2.
FT DOMAIN 199 294 Frame-3.
FT DOMAIN 298 393 Frame-4.
FT DOMAIN 397 492 Frame-5.
FT DOMAIN 496 591 Frame-6.
SQ SEQUENCE 591 AA; 64395 MW; AC8154AD8AGBB280 CRC64;

Query Match 41.1%; Score 134.5; DB 1; Length 591;
Best Local Similarity 50.8%; Pred. No. 2.5e-08;
Matches 30; Conservative 4; Mismatches 20; Indels 5; Gaps 1;

QY 2 EPHTVAAQGVPOHDLGSLQSLPRPKRFSCLILPKIWDYRN-----MNTALIKRNVTP 55
Db 500 ESRVAQAGVQWRDLGSLQPPPGFKRFSCLSPSSWDYRRAPPRPANFCFISRDGVSP 558

RESULT 10
Q6ZNY9 PRELIMINARY; PRT; 122 AA.
AC Q6ZNY9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ26869.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Futsuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
RA Nakaigawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Osuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isogai T., Sugano S.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK130379; BAC85336.1; -.
SQ SEQUENCE 122 AA; 13691 MW; F23AEA08FEF55CB9 CRC64;

Query Match 41.1%; Score 134; DB 2; Length 122;
Best Local Similarity 59.5%; Pred. No. 5.1e-09;
Matches 25; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 MEPHTVAQGVPOHDLGSLQSLPRPKRFSCLILPKIWDYRN 42
Db 67 LKSHVAQAGVQWHDLSLSPQPPPPFKQFSCLSPSSWDYRH 108

RESULT 11
Q8TB48 PRELIMINARY; PRT; 72 AA.
AC Q8TB48;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024651; AAH24651.1; -
DR InterPro; IPR008957; FN_III-like.
KW Hypothetical protein.
SQ SEQUENCE 72 AA; 8162 MW; C14F28BD98E2C1F0 CRC64;

Query Match 41.0%; Score 133.5; DB 2; Length 72;
Best Local Similarity 48.3%; Pred. No. 3.3e-09;
Matches 29; Conservative 4; Mismatches 22; Indels 5; Gaps 1;

Qy 1 MEPTVAQGVQHDLSQSLPRFKRFSCLILPKIWDYRN-----MNTALIKRNYTP 55
Db 1 MESHCIQAQGVQVHGLGLQPPPPKQFSCLSLPSWYDRRAPHLANFCIFRDRGVSP 60

RESULT 12
Q6ZNG3 PRELIMINARY; PRT; 132 AA.
AC Q6ZNG3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ16132.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Suzuki Y.,
RA Sugano S., Nagahori K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK131229; BAD18412.1; -
DR InterPro; IPR004244; Transposase_22.
DR Pfam; PF02994; Transposase_22; 1.
SQ SEQUENCE 132 AA; 15232 MW; E97B0E76F9EB0B3 CRC64;

Query Match 40.6%; Score 132.5; DB 2; Length 132;
Best Local Similarity 52.8%; Pred. No. 8.6e-09;
Matches 28; Conservative 4; Mismatches 16; Indels 5; Gaps 1;

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Qy 8 QAGVQHDLSQSLPRFKRFSCLILPKIWDYRN-----MNTALIKRNYTP 55
Db 67 QAGVQHDLSQSLPRFKRFSCLILPSWYDRRAPHLANFCIFRDRGVSP 119

RESULT 13
Q6ZV58 PRELIMINARY; PRT; 66 AA.
ID Q6ZV58
AC Q6ZV58 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CHP protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bladder;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bladder;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC008373; AAH08373.1; -
SQ SEQUENCE 66 AA; 7409 MW; 77F6F5AFAF7221B3 CRC64;

Query Match 40.5%; Score 132; DB 2; Length 66;
Best Local Similarity 62.8%; Pred. No. 4.7e-09;
Matches 27; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MEPTVAQGVQHDLSQSLPRFKRFSCLILPKIWDYRN 43
Db 1 MESHSVTQAGVQWRDLGSLQPLPPGPKQFQSHLSLPSWYDRRV 43

RESULT 14
Q6ZV58 PRELIMINARY; PRT; 123 AA.
ID Q6ZV58
AC Q6ZV58 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ42963.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Subthalamic nucleus;

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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 45.1791 Seconds
(without alignments)
522.196 Million cell updates/sec

Title: US-10-092-934-9

Perfect score: 326

Sequence: 1 MEPHYVAQGVPOHDLGSLQ.....NMNTALIKRNYPTETGRKS 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1920s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	326	100.0	61	5 AAE29150	Neural th
2	326	100.0	61	6 ABR63248	61 amino
3	326	100.0	61	6 ABU02980	Human neu
4	326	100.0	61	6 ABP59930	Human 61
5	326	100.0	61	6 AAE33197	Neural th
6	326	100.0	61	6 ABJ19453	61-mer ne
7	326	100.0	61	6 ABJ19453	Neural th
8	326	100.0	61	7 ADL37527	Neural th
9	160.5	49.2	124	6 ADL96028	Human neu
10	160.5	49.2	124	6 ABP75466	Human sec
11	160.5	49.2	124	6 ABP75933	Human sec
12	156.5	48.0	73	4 ADI40596	Human pur
13	155	47.5	128	4 AAB64652	Human sec
14	154	47.2	109	7 ADM05537	Human pro
15	154	47.2	134	4 AAU31681	Human pro
16	152	46.6	83	5 ABB98788	Ribosomal
17	150.5	46.2	129	4 AAO00806	Human pol
18	149.5	45.9	73	4 AAE04269	Human gen
19	148.5	45.6	114	7 ADB64269	Human pro
20	148	45.4	115	5 ABP57959	Human gua
21	147.5	45.2	146	6 ABP75894	Human sec
22	147.5	45.2	441	6 ABP75500	Human sec
23	147	45.1	104	7 ADB65611	Human pro
24	147	45.1	151	7 ADC86567	Human GPC
25	146.5	44.9	149	5 AAG80703	Human 2-h

26	146	44.8	112	4 AAU31904	Novel hum
27	144.5	44.3	76	4 AAB75337	Human sec
28	144	44.2	96	5 ABG72220	Pogo tran
29	143	43.9	92	5 ABB99219	Human try
30	142	43.6	218	4 AAE11963	Human C-m
31	141.5	43.4	165	8 ADR08721	Human pro
32	141.5	43.4	165	8 ADR09482	Human pro
33	141	43.3	109	4 AAO07076	Human pol
34	141	43.3	128	4 AAM51382	Human imm
35	140	42.9	54	3 AAG03438	Human sec
36	140	42.9	434	4 AAM93638	Human pol
37	140	42.9	434	8 ADL31456	Human pro
38	140	42.9	440	4 AAU29216	Human PRO
39	140	42.9	440	4 AAB87592	Human PRO
40	140	42.9	440	5 ABG95917	Human sec
41	140	42.9	440	6 ABU58592	Human PRO
42	140	42.9	440	6 ABU88140	Novel hum
43	140	42.9	440	6 ABU84455	Human sec
44	140	42.9	440	6 ABR66329	Human sec
45	140	42.9	440	6 ABR65719	Human sec

ALIGNMENTS

RESULT 1
AAE29150
ID AAE29150 standard; protein; 61 AA.

XX AC AAE29150;

XX XX

DT 27-JAN-2003 (first entry)

XX XX

DE Neural thread protein (NTP) #8.

XX XX

KW Neural thread protein; NTP; hyperplasia; hypertrophy; arteriosclerosis;
KW haemorrhoid; gene therapy; tumour; vascular disease; atherosclerosis;
KW inflammatory disease; nutritional deficiency disease; genetic disease;
KW autoimmune disease; metabolic disease; traumatic disease; intoxication;
KW infectious disease; congenital malformation; enzyme deficiency disease;
KW amyloid disease; fibrosis disease; storage disease; radiation disease;
KW poisoning; environmental disease; endocrine disease; protein therapy;
KW degenerative disease; mechanical disease.

OS Unidentified.

XX XX

PN WO200274323-A2.

XX XX

PD 26-SEP-2002.

XX XX

PF 08-MAR-2002; 2002WO-IB001959.

XX XX

PR 08-MAR-2001; 2001US-0273957P.

XX XX

PA (AVER/) AVERBACK P.

XX XX

PI Averbach P;

XX XX

DR WPI; 2002-759864/82.

XX XX

PT Treating a condition in a patient requiring removal or destruction of

PT cells, such as a benign or malignant tumor of a tissue or an inflammatory

PT disease, comprises administering a neural thread protein (NTP) or a NTP

XX gene to a mammal.

XX PS Claim 23; Fig 9; 70pp; English.

XX XX

CC The invention relates to a method for treating a condition in a patient

CC requiring removal or destruction of cells. The method involves

CC administering to a mammal a neural thread protein (NTP), or administering

CC to a tumour or other target cell a NTP gene, where the expression of the

CC NTP gene is induced resulting in expression of the NTP protein. The

CC method and NTP are useful for treating a condition in a patient requiring

CC removal or destruction of cells, such as a benign or malignant tumour of
CC a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue,
CC preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,
CC bacterially, or parasitically altered tissue, or a malformation of a
CC tissue. Other conditions include a cosmetic modification to a tissue,
CC such as removal of unwanted facial hair, warts or unwanted fatty tissue,
CC a vascular disease, particularly atherosclerosis or arteriosclerosis,
CC hemorrhoids, or varicose veins, an inflammatory disease, autoimmune
CC disease, metabolic disease, hereditary/genetic disease, traumatic disease
CC or physical injury, nutritional deficiency disease, infectious disease,
CC congenital malformation, amyloid disease, fibrosis disease, storage
CC disease, enzyme deficiency disease, poisoning, intoxication, degenerative
CC disease, radiation disease, environmental disease, endocrine disease or
CC mechanical disease. The invention is useful in protein therapy and gene
CC therapy. The present sequence is NTP protein
XX
SQ Sequence 61 AA;

Query Match 100.0%; Score 326; DB 5; Length 61;
Best Local Similarity 100.0%; Pred. No. 9.4e-37;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPHTVAQAGVPOHDLGSLQSLPRFKRFSCLILPKIWDYNNMTALIKENRYTPETGRK 60
Db 1 MEPHTVAQAGVPOHDLGSLQSLPRFKRFSCLILPKIWDYNNMTALIKENRYTPETGRK 60

QY 61 S 61
Db 61 S 61

RESULT 2

ABR63248
ID ABR63248 standard; protein; 61 AA.

AC ABR63248;

DT 28-AUG-2003 (first entry)

DE 61 amino acid neural thread protein.

KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour.

OS Unidentified.

PN W02003008443-A2.

PD 30-JAN-2003.

PF 19-JUL-2002; 2002WO-CA001105.

PR 19-JUL-2001; 2001US-0306150P.

PR 19-JUL-2001; 2001US-0306161P.

PR 16-NOV-2001; 2001US-0331477P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-247999/24.

XX Novel neural thread protein peptide, referred as cell death peptide,
XX useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
XX atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
XX Disclosure; Fig 9; 77pp; English.

XX The present invention relates to a neural thread protein (NTP) peptide
XX referred to as cell death peptide. Thought to be cytostatic,
XX antibacterial, immunosuppressive and antiinflammatory. It is useful for
XX treating a condition in a patient requiring removal or destruction of
XX cells, for treating a condition such as benign or malignant tumor,

CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for
CC a pancreatic thread protein. The peptide is conjugated, linked or bound
CC to a molecule chosen from antibody or its fragment, antibody-like binding
CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side
CC effects of surgery. The present sequence is an NTP amino acid sequence
XX
SQ Sequence 61 AA;

Query Match 100.0%; Score 326; DB 6; Length 61;
Best Local Similarity 100.0%; Pred. No. 9.4e-37;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPHTVAQAGVPOHDLGSLQSLPRFKRFSCLILPKIWDYNNMTALIKENRYTPETGRK 60
Db 1 MEPHTVAQAGVPOHDLGSLQSLPRFKRFSCLILPKIWDYNNMTALIKENRYTPETGRK 60

QY 61 S 61
Db 61 S 61

RESULT 3

ABU02980

ID ABU02980 standard; protein; 61 AA.

AC ABU02980;

DT 20-JAN-2003 (first entry)

DE Human neural thread protein AD7C-NTP, protein fragment #8.

KW Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;
KW transplantation; grafting; chemotherapy; immunotherapy; vaccination;
KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;
KW radiation; tumour; hyperplasia; hypertrophy; overgrowth of tissue;
KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;
KW cosmetic modification; vascular disease; atherosclerosis;
KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;
KW autoimmune disease; metabolic disease; traumatic disease;
KW physical injury; nutritional deficiency disease; infectious disease;
KW amyloid disease; fibrosis disease; storage disease;
KW congenital malformation; enzyme deficiency disease; poisoning;
KW intoxication; environmental disease; radiation disease;
KW endocrine disease; degenerative disease; mechanical disease.

XX Homo sapiens.

XX OS WO200297030-A2.

XX PN 05-DEC-2002.

XX XX 24-MAY-2002; 2002WO-CA0000759.

XX XX 25-MAY-2001; 2001US-0293156P.

XX (NYMO-) NYMOX CORP.

XX PA Averbach PA;

XX PI WPI; 2003-041406/03.

XX Novel peptides similar in amino acid sequence to neural thread proteins
XX (NTP), useful for treating unwanted cellular proliferations such as
XX malignant tumors and prostatic hyperplasia.

XX Disclosure; Fig 9; 78pp; English.

XX The invention describes an NTP-peptide (1) comprising at least one amino
XX acid sequence corresponding to part of the amino acid sequence of a
XX neural thread protein, AD7C-NTP. The invention provides a method of

CC treating a condition requiring removal or destruction of cells of a
CC mammal comprising administering to a mammal, a therapeutic amount of (I).
CC The treatment is administered to the mammal before, during or after
CC surgical excision, transplantation, grafting, chemotherapy,
CC immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,
CC laser therapy, phototherapy, gene therapy and/or radiation. The method is
CC useful for treatment of benign or malignant tumour; hyperplasia,
CC hypertrophy or overgrowth of tissue; virally, bacterially or
CC parasitically altered tissue; malformation of tissue selected from lung,
CC breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,
CC sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary
CC gland, blood, brain and its coverings, spinal cord, muscle, connective
CC tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary,
CC reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,
CC tonsils, mouth and lymph nodes and lymphoid system; tonsillary
CC hypertrophy; prostatic hyperplasia; cosmetic modification to a tissue;
CC vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;
CC varicose veins; inflammatory disease; autoimmune disease; metabolic
CC disease; hereditary/genetic disease; traumatic disease; physical injury;
CC nutritional deficiency disease; infectious disease; amyloid disease;
CC fibrosis disease; storage disease; congenital malformation; enzyme
CC deficiency disease; poisoning; intoxication; environmental disease;
CC radiation disease; endocrine disease; degenerative disease and mechanical
CC disease. This is the amino acid sequence of a human neural thread protein
CC AD7C-NTP protein fragment
XX
SQ Sequence 61 AA;

Query Match 100.0%; Score 326; DB 6; Length 61;
Best Local Similarity 100.0%; Pred. No. 9.4e-37;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPTVAQAGVPOHDLGSLQSLPRFRFSCILLPKIWDYRNMTALIKRNYTPETGRK 60
Db 1 MEPTVAQAGVPOHDLGSLQSLPRFRFSCILLPKIWDYRNMTALIKRNYTPETGRK 60

Qy 61 S 61
Db 61 S 61

RESULT 4

ABP59930
ID ABP59930 standard; protein; 61 AA.

XX
AC ABP59930;

XX
DT 08-SEP-2003 (first entry)

XX Human 61 amino acid neural thread protein-like protein.

XX Human; tumour; cancer; neural thread protein; NTP; cell removal;
KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;
KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;
KW gene therapy.

XX Homo sapiens.

XX WO2003044053-A2.

XX 30-MAY-2003.

XX 18-NOV-2002; 2002WO-CA001757.

XX 16-NOV-2001; 2001US-0331477P.

XX (NYMO-) NYMOX CORP.

XX Averbach P, Gemmell J;

XX WPI; 2003-457592/43.

XX New neural thread protein (NTP), useful for preparing a composition for

PT treating or preventing a condition in a mammal requiring removal or
PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or
XX inflammatory disease.

XX Disclosure; Fig 7; 98pp; English.

XX The present invention relates to peptides derived from the human neural
CC thread protein (NTP). The peptides are useful for preparing a composition
CC for treating or preventing a condition in a mammal requiring removal or
CC destruction of cells, comprising tonsillary hypertrophy, prostatic
CC hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a
CC breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,
CC varicose veins, atherosclerosis, inflammatory, metabolic, infectious,
CC fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,
CC occlusion or blockage of an artery or of a stent placed or implanted in
CC an artery. The present sequence is an NTP protein used to produce
CC peptides of the invention

XX SQ Sequence 61 AA;

Query Match 100.0%; Score 326; DB 6; Length 61;

Best Local Similarity 100.0%; Pred. No. 9.4e-37;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPTVAQAGVPOHDLGSLQSLPRFRFSCILLPKIWDYRNMTALIKRNYTPETGRK 60

Db 1 MEPTVAQAGVPOHDLGSLQSLPRFRFSCILLPKIWDYRNMTALIKRNYTPETGRK 60

Qy 61 S 61

Db 61 S 61

RESULT 5

AAE33197
ID AAE33197 standard; protein; 61 AA.

XX
AC AAE33197;

XX 16-APR-2003 (first entry)

XX Neural thread protein (NTP) #8.

XX Cell death; tissue necrosis; neural thread protein; NTP; amyloidosis;
KW stroke; brain tumour; Pick's disease; Parkinson's disease; glaucoma;
KW Alzheimer's disease; gene therapy.

XX Unidentified.

XX WO200289841-A2.

XX 14-NOV-2002.

XX 06-MAY-2002; 2002WO-CA000681.

XX 04-MAY-2001; 2001US-0288463P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-120506/11.

XX Preventing, controlling, modulating, ameliorating and/or treating cell
PT death or tissue necrosis using antibodies to neural thread proteins,
PT useful in disorders such as stroke, brain tumor, glaucoma and Alzheimer's
PT disease.

XX Disclosure; Fig 12; 60pp; English.

XX The invention relates to a method of preventing, and/or inhibiting cell
CC death and/or tissue necrosis in live tissue containing neural thread
CC proteins (NTP). The method involves contacting the live tissue with at

CC least one antibody, fragment or derivative that recognises NTP, where the
 CC antibody, fragment or derivative is present to prevent, control,
 CC ameliorate and/or inhibit cell death and/or tissue necrosis caused by the
 CC presence of NTP. Methods and compositions of the invention are useful for
 CC preventing, modulating, controlling and/or treating disorders associated
 CC with cell death and/or tissue necrosis such as stroke, brain tumour,
 CC Pick's disease, Parkinson's disease, amyloidosis, Glaucoma and
 CC Alzheimer's disease. The invention is useful in gene therapy. The present
 CC sequence is NTP protein

XX
 SQ Sequence 61 AA;

Query Match 100.0%; Score 326; DB 6; Length 61;
 Best Local Similarity 100.0%; Pred. NO. 9.4e-37;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPTVAQAGVQPHDLSLQSLPRFKRFSCLLPKIKWDYRNMMNTALIKENRYTPETGRK 60
 |||||
 DB 1 MEPTVAQAGVQPHDLSLQSLPRFKRFSCLLPKIKWDYRNMMNTALIKENRYTPETGRK 60
 |||||
 QY 61 S 61
 |
 DB 61 S 61

RESULT 6
 ABJ19453
 ID ABJ19453 standard; protein; 61 AA.

XX AC ABJ19453;

XX DT 27-MAR-2003 (first entry)

XX DE 61-mer neural thread protein.

XX KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
 KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.

XX OS Unidentified.

XX PN WO200292115-A2.

XX PD 21-NOV-2002.

XX PF 16-MAY-2002; 2002WO-CA000712.

XX PR 16-MAY-2001; 2001US-0290971P.

XX PA (NYMO-) NYMOX CORP.

XX PI Averbach PA;

XX DR WPI; 2003-129234/12.

XX PT Preventing and/or inhibiting cell death and/or tissue necrosis in a
 PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
 PT disease, by contacting the live tissue with at least one segment of
 PT neural thread proteins (NTP).

PS Disclosure; Fig 9; 60pp; English.

XX The invention relates to a novel method for preventing and/or inhibiting
 CC cell death and/or tissue necrosis in a tissue comprising contacting the
 CC live tissue with at least one segment of neural thread proteins (NTP).
 CC The methods are composition are useful for treating a neurodegenerative
 CC disorder, such as Alzheimer's disease. This sequence represents an NTP
 CC protein of the invention

XX SQ Sequence 61 AA;

Query Match 100.0%; Score 326; DB 6; Length 61;
 Best Local Similarity 100.0%; Pred. NO. 9.4e-37;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPTVAQAGVQPHDLSLQSLPRFKRFSCLLPKIKWDYRNMMNTALIKENRYTPETGRK 60
 |||||
 DB 1 MEPTVAQAGVQPHDLSLQSLPRFKRFSCLLPKIKWDYRNMMNTALIKENRYTPETGRK 60
 |||||
 QY 61 S 61
 |
 DB 61 S 61

RESULT 7
 ADB37527

ID ADB37527 standard; protein; 61 AA.

XX AC ADB37527;

XX DT 04-DEC-2003 (first entry)

XX DE Neural thread protein-like protein #3.

XX KW Cytostatic; Antitumour; Antipsoriatic; Dermatological;
 KW Antiatherosclerotic; Antiarteriosclerotic; Vasotropic; Antiinflammatory;
 KW Immunosuppressive; Tranquillizer; Antiemetic; Virucide; AD7c-NTP;
 KW neural thread protein; neuritic sprouting.

XX OS Unidentified.

XX PN WO2003008444-A2.

XX PD 30-JAN-2003.

XX PF 19-JUL-2002; 2002WO-CA001106.

XX PR 19-JUL-2001; 2001US-0306150P.

XX PR 19-JUL-2001; 2001US-0306161P.

XX PR 16-NOV-2001; 2001US-0331477P.

XX PA (NYMO-) NYMOX CORP.

XX PI Averbach PA, Gemmell J;

XX DR WPI; 2003-248000/24.

XX PT Novel Related peptide or AD7c-neural thread peptide, useful for treating
 PT unwanted cellular proliferations, glandular hyperplasia, unwanted facial
 PT hair, warts and unwanted fatty tissue.

PS Disclosure; Fig 9; 109pp; English.

XX The present invention relates to AD7c-neural thread protein (NTP) and
 CC related proteins and peptides (I; ADB37528-ADB37641). The sequences are
 CC useful for treating a condition in a patient requiring removal or
 CC destruction of cells. The condition can be selected from benign or
 CC malignant tumour of a tissue, hyperplasia, hypertrophy or overgrowth of a
 CC tissue, virally, bacterially or parasitically altered tissue, or
 CC malformation of a tissue, where the tissue is selected from lung, breast,
 CC stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney, sinus,
 CC colon, intestine, stomach, rectum, oesophagus, heart, spleen, salivary
 CC gland, blood, brain and its coverings, spinal cord and its coverings,
 CC muscle, connective tissue, adrenal, parathyroid, thyroid, uterus, testis,
 CC pituitary, reproductive organs, liver, gall bladder, eye, ear, nose,
 CC throat, tonsils, mouth, lymph nodes and lymphoid tissue. The condition is
 CC preferably tonsillary hypertrophy, prostatic hyperplasia, psoriasis,
 CC eczema, dermatosis, cosmetic modification to a tissue (skin, eye, ear,
 CC nose, throat, mouth, muscle, connective, hair or breast tissue), varicose
 CC disease (atherosclerosis or arteriosclerosis), haemorrhoids, varicose
 CC veins, inflammatory disease, autoimmune disease, metabolic disease,
 CC hereditary/genetic disease, traumatic disease or physical injury,
 CC nutritional deficiency disease, infectious disease, amyloid disease,
 CC fibrosis disease, storage disease, congenital malformation, enzyme
 CC deficiency disease, poisoning, intoxication, environmental disease,
 CC radiation disease, endocrine disease, degenerative disease and mechanical
 CC disease. The peptides are useful for treating unwanted cellular

CC proliferations, glandular (e.g. prostate) hyperplasia, unwanted facial
 CC hair, warts and unwanted fatty tissue, or for preparing antibodies that
 CC recognize and/or bind to Related proteins, Related peptides or NTP
 CC peptides. The present sequence was used to illustrate the invention.
 XX
 SQ Sequence 61 AA;
 Query Match 100.0%; Score 326; DB 7; Length 61;
 Best Local Similarity 100.0%; Pred. NO. 9.4e-37; Mismatches 0; Indels 0; Gaps 0;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEPTVAQAGVPOHDLGSLQSLPRFRFSCILIPKIWDYRNMTALIKENRYTPETGRK 60
 Db 1 MEPTVAQAGVPOHDLGSLQSLPRFRFSCILIPKIWDYRNMTALIKENRYTPETGRK 60
 QY 61 S 61
 Db 61 S 61
 RESULT 8
 ADL96028
 ID ADL96028 standard; protein; 61 AA.
 AC ADL96028;
 DT 20-MAY-2004 (first entry)
 DE Human neural thread protein, NTP61.
 KW Human; neural thread protein; NTP122; NTP112; NTP106; NTP98; NTP75;
 KW NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;
 KW eczema; haemorrhoid; atherosclerosis; inflammatory disease;
 KW autoimmune disease; metabolic disease; hereditary disease;
 KW genetic disease; traumatic disease; physical injury;
 KW nutritional deficiency disease; infectious disease; amyloid disease;
 KW Alzheimer's disease; storage disease; congenital malformation;
 KW enzyme deficiency disease; poisoning; intoxication;
 KW environmental disease; radiation disease; endocrine disease;
 KW degenerative disease; mechanical disease.
 XX
 OS Homo sapiens.
 XX
 PN US2003166569-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 15-NOV-2002; 2002US-00294891.
 XX
 PR 16-NOV-2001; 2001US-0331477P.
 XX
 PA (AVER/) AVERBACK P.
 PA (GEMM/) GEMMELL J.
 XX
 PI Averbach P, Gemmell J;
 XX
 DR WPI; 2003-898099/82.
 XX
 PT New neural thread protein or its variants, useful for treating tumors and
 PT other conditions requiring the removal or destruction of cells (e.g.
 PT prostatic hyperplasia, psoriasis, eczema, hemorrhoids or
 PT atherosclerosis).
 XX
 PS Disclosure; SEQ ID NO 7; 32pp; English.
 XX
 CC The invention relates to a peptide, or its homologue, derivative,
 CC fragment, variant or mimetic, comprising at least one neural thread
 CC protein (NTP) peptide appearing as ADL96029-ADL96069, derived from
 CC NTP122, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid
 CC encoding an amino acid sequence corresponding to the above peptide, a
 CC composition comprising one or more peptides or nucleic acids cited above
 CC and a carrier, a method of treating a condition in a mammal requiring
 CC removal or destruction of cells (comprising administering to the mammal

CC an amount of the peptide cited above) and a method of preventing or
 CC inhibiting the stenosis, occlusion or blockage of a stent, comprising
 CC coating the stent with an amount of the above peptide. The peptide
 CC further comprises an amino acid in a reverse-D order based on the above
 CC amino acid sequences. The composition and methods are useful in treating
 CC tumours and other conditions requiring the removal or destruction of
 CC cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or
 CC atherosclerosis). These may also be used in treating inflammatory or
 CC diseases, autoimmune diseases, metabolic diseases, hereditary/genetic
 CC diseases, traumatic diseases or physical injuries, nutritional deficiency
 CC diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,
 CC storage diseases, congenital malformation, enzyme deficiency diseases,
 CC poisoning, intoxication, environmental diseases, radiation diseases,
 CC endocrine diseases, degenerative diseases or mechanical diseases. The
 CC present sequence is a human NTP protein from which the peptides of the
 XX invention are derived.
 SQ Sequence 61 AA;
 Query Match 100.0%; Score 326; DB 7; Length 61;
 Best Local Similarity 100.0%; Pred. NO. 9.4e-37; Mismatches 0; Indels 0; Gaps 0;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEPTVAQAGVPOHDLGSLQSLPRFRFSCILIPKIWDYRNMTALIKENRYTPETGRK 60
 Db 1 MEPTVAQAGVPOHDLGSLQSLPRFRFSCILIPKIWDYRNMTALIKENRYTPETGRK 60
 QY 61 S 61
 Db 61 S 61
 RESULT 9
 ABP75466
 ID ABP75466 standard; protein; 124 AA.
 AC ABP75466;
 XX
 DT 10-FEB-2003 (first entry)
 XX
 DE Human secretory polypeptide SPTM SEQ ID NO 650.
 XX
 KW Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;
 KW asthma; Crohn's disease; neurological disorder; epilepsy; cancer;
 KW Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;
 KW multiple sclerosis; Parkinson's disease; cell proliferative disorder;
 KW anti-inflammatory; immunosuppressive; neuroprotective; neurotropic;
 KW neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic;
 KW antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus;
 KW secretory polynucleotide; secretory protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200283876-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 27-MAR-2002; 2002WO-US0009921.
 XX
 PR 29-MAR-2001; 2001US-0280067P.
 PR 29-MAR-2001; 2001US-0280068P.
 PR 16-MAY-2001; 2001US-0291280P.
 PR 17-MAY-2001; 2001US-0291829P.
 PR 17-MAY-2001; 2001US-0291849P.
 PR 19-JUN-2001; 2001US-0299428P.
 PR 20-JUN-2001; 2001US-0299776P.
 PR 20-JUN-2001; 2001US-0300001P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
 PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleeferd Y, Gerstin EH;

PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 XX Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
 DR WPI: 2003-075543/07.
 DR N-PSDB; ABZ35914.
 XX New human secretory proteins and polynucleotides, useful for diagnosing,
 PT treating or preventing autoimmune/inflammatory disorders (e.g. AIDS),
 PT neurological disorders (e.g. Alzheimer's), or cell proliferations or
 PT cancers.
 XX Claim 27; SEQ ID NO 650; 458pp + Sequence Listing; English.
 XX The invention relates to a secretory polynucleotide (designated sptm)
 CC comprising any of 567 polynucleotide sequences (ABZ35837-ABZ36403), a
 CC naturally occurring polynucleotide sequence at least 90 % identical to
 CC the polynucleotide sequence, a polynucleotide complementary to them or an
 CC RNA equivalent of them. The polypeptide or polynucleotide are useful for
 CC treating, preventing or diagnosing a disease or condition associated with
 CC the expression of functional SPTM. These are particularly useful for
 CC diagnosing, treating or preventing autoimmune/inflammatory disorders
 CC (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's
 CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,
 CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,
 CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,
 CC schizophrenia or amnesia), or cell proliferative disorders (e.g.
 CC psoriasis, polycythemia vera, or cancers including adenocarcinoma,
 CC leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,
 CC breast, cervix or prostate). The present sequence is one of the SPTM
 CC proteins of the invention (ABP75384-ABP75962). Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 124 AA;
 SQ Query Match 49.2%; Score 160.5; DB 6; Length 124;
 Best Local Similarity 57.9%; Pred. No. 1.1e-13;
 Matches 33; Conservative 6; Mismatches 13; Indels 5; Gaps 1;
 QY 1 MEPHTVAQGVQPHDGLGSLQSLPRFRKFSCLILPKIWDYR-----NMNTALIKRNR 52
 Db 28 MKSHSVAQAGVQWCDLGLSLQPLLPFRKFSCLTIPSSWDYRCTPCPVNFCIFSRDR 84
 RESULT 10
 ABP75933
 ID ABP75933 standard; protein; 124 AA.
 XX ABP75933;
 XX 10-FEB-2003 (first entry)
 DE Human secretory polypeptide SPTM SEQ ID NO 1117.
 XX Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;
 XX asthma; Crohn's disease; neurological disorder; epilepsy; cancer;
 KW Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;
 KW multiple sclerosis; Parkinson's disease; cell proliferative disorder;
 KW anti-inflammatory; immunosuppressive; neuroprotective; nontropic;
 KW neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic;
 KW antipsoriatic; anti-anaemic; anti-HIV; human immunodeficiency virus;
 KW secretory polynucleotide; secretory protein.
 XX Homo sapiens.
 OS WO200283876-A2.
 XX 24-OCT-2002.
 PD 27-MAR-2002; 2002WO-US009921.
 XX 29-MAR-2001; 2001US-0280067P.

PR 29-MAR-2001; 2001US-0280068P.
 PR 16-MAY-2001; 2001US-0291280P.
 PR 17-MAY-2001; 2001US-0291829P.
 PR 17-MAY-2001; 2001US-0291849P.
 PR 19-JUN-2001; 2001US-0299428P.
 PR 20-JUN-2001; 2001US-0299776P.
 PR 20-JUN-2001; 2001US-030001P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Daffour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Anshey SR;
 PI Doughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
 XX WPI: 2003-075543/07.
 DR N-PSDB; ABZ36375.
 DR New human secretory proteins and polynucleotides, useful for diagnosing,
 XX treating or preventing autoimmune/inflammatory disorders (e.g. AIDS),
 XX neurological disorders (e.g. Alzheimer's), or cell proliferations or
 PT cancers.
 PT Claim 27; SEQ ID NO 1117; 458pp + Sequence Listing; English.
 XX The invention relates to a secretory polynucleotide (designated sptm)
 CC comprising any of 567 polynucleotide sequences (ABZ35837-ABZ36403), a
 CC naturally occurring polynucleotide sequence at least 90 % identical to
 CC the polynucleotide sequence, a polynucleotide complementary to them or an
 CC RNA equivalent of them. The polypeptide or polynucleotide are useful for
 CC treating, preventing or diagnosing a disease or condition associated with
 CC the expression of functional SPTM. These are particularly useful for
 CC diagnosing, treating or preventing autoimmune/inflammatory disorders
 CC (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's
 CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,
 CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,
 CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,
 CC schizophrenia or amnesia), or cell proliferative disorders (e.g.
 CC psoriasis, polycythemia vera, or cancers including adenocarcinoma,
 CC leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,
 CC breast, cervix or prostate). The present sequence is one of the SPTM
 CC proteins of the invention (ABP75384-ABP75962). Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 124 AA;
 SQ Query Match 49.2%; Score 160.5; DB 6; Length 124;
 Best Local Similarity 57.9%; Pred. No. 1.1e-13;
 Matches 33; Conservative 6; Mismatches 13; Indels 5; Gaps 1;
 QY 1 MEPHTVAQGVQPHDGLGSLQSLPRFRKFSCLILPKIWDYR-----NMNTALIKRNR 52
 Db 28 MKSHSVAQAGVQWCDLGLSLQPLLPFRKFSCLTIPSSWDYRCTPCPVNFCIFSRDR 84
 RESULT 11
 ADI40596
 ID ADI40596 standard; protein; 124 AA.
 XX ADI40596;
 XX 22-APR-2004 (first entry)
 DT Human purified secretory polypeptide (SPTM), seq id 289.
 XX Antiartherosclerotic; antipsoriatic; cytostatic; secretory molecule;
 KW agonist; antagonist; gene therapy; antisense; human; secretory;
 KW purified secretory polynucleotide; sptm; toxicity; arteriosclerosis;
 KW psoriasis; cancer.

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OS Homo sapiens.
XX WO2003062385-A2.
XX 31-JUL-2003.
XX 15-JAN-2003; 2003WO-US001605.
XX 17-JAN-2002; 2002US-0349413P.
XX 17-JAN-2002; 2002US-0349946P.
XX (INCY-) INCYTE GENOMICS INC.
PA (JONE/) JONES A L.
PA (DAHL/) DAHL C R.
PA (GIET/) GIETZEN D.
PA (CHIN/) CHINN J.
PA (DUFO/) DUFOUR G E.
PA (JACK/) JACKSON J L.
PA (YUJY/) YU J Y.
PA (TUAS/) TUASON O.
PA (YAPP/) YAP P E.
PA (AMSH/) AMSHEY S R.
PA (DAMT/) DAM T C.
PA (LIUT/) LIU T F.
PA (GERS/) GERSTIN E H.
PA (PERA/) PERALTA C H.
PA (LEWI/) LEWIS S A.
PA (CHEN/) CHEN A J.
PA (MARW/) MARWAHA R.
PA (LANR/) LAN R Y.
PA (URAS/) URASHKA M E.
PA (KRIS/) KRISTNAM S R.
PA (KOLL/) KOLLURU V.
PA (PANE/) PANESAR I S.
XX Jones AL, Dahl CR, Gietzen D, Chinn J, Dufour GE, Jackson JL,
PI Yu JY, Tuason O, Yap PE, Amshey SR, Dam TC, Liu TF, Gerstin EH;
PI Peralta CH, Lewis SA, Chen AJ, Marwaha R, Lan RY, Urashka ME;
PI Kristnam SR, Kolluru V, Panesar IS;
XX WPI; 2003-853444/79.
DR N-PSDB; ADI40433.
XX New isolated secreted polynucleotide for diagnosing or treating
PT conditions, diseases or disorders associated with cell signaling e.g.
PT arteriosclerosis, psoriasis, and cancer.
XX Claim 27a; SEQ ID NO 289; 486pp; English.
XX The invention relates to isolated purified secreted polynucleotides
CC (sptm) (I), and the polypeptides (SPTM) encoded by sptm. A polypeptide
CC encoded by (I) is used to identify a compound which binds to it. A
CC microarray comprising (I) is used to generate a transcript. (I) is used
CC to screen a compound for effectiveness in altering expression of (I). (I)
CC is used to assess toxicity of a test compound. An agonist or antagonist
CC identified by a new method is used in a pharmaceutical composition. The
CC secretory molecules are used to diagnose or treat conditions, diseases or
CC disorders associated with cell signaling e.g. arteriosclerosis,
CC psoriasis, and cancer. Sequences given in ADI40308-ADI40468 represent
CC human purified secretory polynucleotides of the invention, and those
CC given in ADI40469-ADI40631 represent the polypeptides they encode.
XX Sequence 124 AA;
SQ Query Match 49.2%; Score 160.5; DB 7; Length 124;
Best Local Similarity 57.9%; Pred. No. 1.1e-13;
Matches 33; Conservative 6; Mismatches 13; Indels 5; Gaps 1;
Oy 1 MEPTVAQAGVPQHDLSLQSLPRFKRFSCLILPKIWDYR-----NNNTALIKRNR 52
Db 28 MKSHVAQAGVQWCDLGLSLQPLPRFKRFSCLITPSSWDYRCTTPCPVNFCIFSRDR 84
RESULT 12
AAB64652
ID AAB64652 standard; protein; 73 AA.
XX
AC AAB64652;
XX
DT 22-MAR-2001 (first entry)
XX Human secreted protein BLAST search protein SEQ ID NO: 162.
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX Homo sapiens.
OS
XX WO2000077197-A1.
XX 21-DEC-2000.
XX 01-JUN-2000; 2000WO-US014934.
XX 11-JUN-1999; 99US-0138599P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (ROSE/) ROSEN C A.
XX Rosen CA, Ruben SM, Komatsoulis GA;
PI WPI; 2001-032312/04.
XX Isolated nucleic acid molecule encoding a human secreted protein is used
PT in preventing, treating or ameliorating a medical condition.
XX Disclosure; Page 540-541; 558pp; English.
XX The invention relates to the isolation of genes AAF32757-F32803 encoding
CC the human secreted proteins AAB64549-B64594. The sequence is used as a
CC query sequence for doing BLASTX searches to identify homologous
CC sequences. The genes and proteins are useful for preventing, ameliorating
CC or treating medical conditions, e.g. by protein or gene therapy. The
CC genes are isolated from a range of human tissues disclosed in the
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
CC e.g. breast and ovarian cancer, and other cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d)
CC wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections
XX Sequence 73 AA;
SQ Query Match 48.0%; Score 156.5; DB 4; Length 73;
Best Local Similarity 55.0%; Pred. No. 2.1e-13;
Matches 33; Conservative 6; Mismatches 16; Indels 5; Gaps 1;
Oy 1 MEPTVAQAGVPQHDLSLQSLPRFKRFSCLILPKIWDYRNMNT-----ALIKRNYTP 55
Db 2 MESHVAQAGVQWHLGLSLQPLPGFKXFXSCLSLPSRWDYRHVLTHPADFCIFSRDRVLP 61
RESULT 13
ADM05537
ID ADM05537 standard; protein; 128 AA.
XX
AC ADM05537;
XX
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DT 20-MAY-2004 (first entry)
DE Human protein of the invention SEQ ID NO:4222.
XX human; gene therapy; diagnostic marker; pharmaceutical.
XX Homo sapiens.
XX EP1347046-A1.
XX 24-SEP-2003.
XX 12-APR-2002; 2002EP-00008400.
XX 22-MAR-2002; 2002JP-00137785.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX WPI; 2003-723558/69.
DR N-PSDB; ADM03094.
XX New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX Claim 1; SEQ ID NO 4222; 305pp; English.
XX The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.
XX Sequence 128 AA;
SQ
Query Match 47.5%; Score 155; DB 7; Length 128;
Best Local Similarity 71.4%; Pred. No. 6.5e-13;
Matches 30; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MEPHTVAQGVPOHDLGSLQSLPRFRKFSCLILPKIWDYRN 42
|:|||||:|||||:|||||:|||||:|||||:
Db 1 MGTHVAQGVQVRHDLGSLQLPPPRFRKFSCLSLPSSWDYRH 42

RESULT 14
ADM06040
ID ADM06040 standard; protein; 109 AA.
XX AC ADM06040;
XX 20-MAY-2004 (first entry)
XX Human protein of the invention SEQ ID NO:4725.
DE Human; gene therapy; diagnostic marker; pharmaceutical.
XX Homo sapiens.
XX EP1347046-A1.
XX 24-SEP-2003.
XX 12-APR-2002; 2002EP-00008400.
XX PT vaccination, testing and therapy.
XX

22-MAR-2002; 2002JP-00137785.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX WPI; 2003-723558/69.
DR N-PSDB; ADM03597.
XX New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX Claim 1; SEQ ID NO 4725; 305pp; English.
XX The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.
XX Sequence 109 AA;
SQ
Query Match 47.2%; Score 154; DB 7; Length 109;
Best Local Similarity 81.1%; Pred. No. 7.4e-13;
Matches 30; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 6 VAQAGVPOHDLGSLQSLPRFRKFSCLILPKIWDYRN 42
|:|||||:|||||:|||||:|||||:|||||:
Db 29 VAQAGVQVHDLGSLQLPPLPRFRKFSCLSLPSSWDYRH 65

RESULT 15
AAU31681
ID AAU31681 standard; protein; 134 AA.
XX AC AAU31681;
XX 18-DEC-2001 (first entry)
XX Novel human secreted protein #2172.
DE Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX Homo sapiens.
XX WO200179449-A2.
XX 25-OCT-2001.
XX 16-APR-2001; 2001WO-US008656.
XX 18-APR-2000; 2000US-00552929.
PR 26-JAN-2001; 2001US-00770160.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
PI WPI; 2001-611725/70.
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
XX

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PS Claim 20; Page 496; 765pp; English.

The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukemias. AAU29510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.

Sequence 134 AA;

Query Match	47.2%	Score 154;	DB 4;	Length 134;
Best Local Similarity	75.0%;	Pred. No. 9.4e-13;		
Matches 30;	Conservative	1;	Mismatches 9;	Indels 0;
				Gaps 0;

Qy 2 EPHTVAQAGVPQHDLSQLSLPRFKRFSCLILPKIWDR 41
| | | | | | | | | | | | | | | | | | | | | |
: | | | | | | | | | | | | | | | | | | | | |
Db 58 ESHSVAQAEVQVHDLSQLSLTPRFKRFSCLSIPSRWDR 97
| | | | | | | | | | | | | | | | | | | | | |

Search completed: October 11, 2005, 07:11:16
Job time : 47.1791 secs

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US-10-146-130-10

; Sequence 10, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-10

Query Match 100.0%; Score 326; DB 14; Length 61;
Best Local Similarity 100.0%; Pred. No. 1e-36;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPHTVAQAGVPQHDLSQSLPRFKRFSCLILPKIWDYRNMMNTALIKENRYTPETGRK 60
Db 1 MEPHTVAQAGVPQHDLSQSLPRFKRFSCLILPKIWDYRNMMNTALIKENRYTPETGRK 60

Qy 61 S 61
Db 61 S 61

RESULT 3
US-10-092-934-9
; Sequence 9, Application US/10092934
; Publication No. US20030054990A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHODS OF USING NEURAL THREAD PROTEINS TO TREAT TUMORS
; TITLE OF INVENTION: AND CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; FILE REFERENCE: 018792-0199
; CURRENT APPLICATION NUMBER: US/10/092,934
; CURRENT FILING DATE: 2002-06-05
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-934-9

Query Match 100.0%; Score 326; DB 14; Length 61;
Best Local Similarity 100.0%; Pred. No. 1e-36;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPHTVAQAGVPQHDLSQSLPRFKRFSCLILPKIWDYRNMMNTALIKENRYTPETGRK 60
Db 1 MEPHTVAQAGVPQHDLSQSLPRFKRFSCLILPKIWDYRNMMNTALIKENRYTPETGRK 60

Qy 61 S 61
Db 61 S 61

RESULT 4
US-10-153-334-9
; Sequence 9, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF

; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003-000006
; CURRENT APPLICATION NUMBER: US/10/153,334
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,156
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-334-9

Query Match 100.0%; Score 326; DB 14; Length 61;
Best Local Similarity 100.0%; Pred. No. 1e-36;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPHTVAQAGVPQHDLSQSLPRFKRFSCLILPKIWDYRNMMNTALIKENRYTPETGRK 60
Db 1 MEPHTVAQAGVPQHDLSQSLPRFKRFSCLILPKIWDYRNMMNTALIKENRYTPETGRK 60

Qy 61 S 61
Db 61 S 61

RESULT 5
US-10-198-069-9
; Sequence 9, Application US/10198069
; Publication No. US20030096756A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; FILE REFERENCE: 59003.000009
; CURRENT APPLICATION NUMBER: US/10/198,069
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-069-9

Query Match 100.0%; Score 326; DB 14; Length 61;
Best Local Similarity 100.0%; Pred. No. 1e-36;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPHTVAQAGVPQHDLSQSLPRFKRFSCLILPKIWDYRNMMNTALIKENRYTPETGRK 60
Db 1 MEPHTVAQAGVPQHDLSQSLPRFKRFSCLILPKIWDYRNMMNTALIKENRYTPETGRK 60

Qy 61 S 61
Db 61 S 61

RESULT 6
US-10-198-070-9
; Sequence 9, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMELL, JACK

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; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR FILING DATE: 2002-07-19
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-070-9

Query Match      100.0%; Score 326; DB 14; Length 61;
Best Local Similarity 100.0%; Pred. No. 1e-36;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPHTVAQGVPOHDLGSLQSLPRFKRFSCLILPKIWDYRNMTALIKRNRYPETGRK 60
Db 1 MEPHTVAQGVPOHDLGSLQSLPRFKRFSCLILPKIWDYRNMTALIKRNRYPETGRK 60

Qy 61 S 61
Db 61 S 61

RESULT 7
US-10-294-891-7
; Sequence 7, Application US/10294891
; Publication No. US20030168569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-7

Query Match      100.0%; Score 326; DB 14; Length 61;
Best Local Similarity 100.0%; Pred. No. 1e-36;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPHTVAQGVPOHDLGSLQSLPRFKRFSCLILPKIWDYRNMTALIKRNRYPETGRK 60
Db 1 MEPHTVAQGVPOHDLGSLQSLPRFKRFSCLILPKIWDYRNMTALIKRNRYPETGRK 60

Qy 61 S 61
Db 61 S 61

RESULT 8
US-10-920-313-7
; Sequence 7, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
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; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-7

Query Match      100.0%; Score 326; DB 17; Length 61;
Best Local Similarity 100.0%; Pred. No. 1e-36;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPHTVAQGVPOHDLGSLQSLPRFKRFSCLILPKIWDYRNMTALIKRNRYPETGRK 60
Db 1 MEPHTVAQGVPOHDLGSLQSLPRFKRFSCLILPKIWDYRNMTALIKRNRYPETGRK 60

Qy 61 S 61
Db 61 S 61

RESULT 9
US-10-108-260A-4222
; Sequence 4222, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4222
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4222

Query Match      47.5%; Score 155; DB 15; Length 128;
Best Local Similarity 71.4%; Pred. No. 6.4e-13;
Matches 30; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MEPHTVAQGVPOHDLGSLQSLPRFKRFSCLILPKIWDYRN 42
Db 1 MGTHSVAQGVQVRHDLGSLQSLPRFKRFSCLILPSSWDYR 42

RESULT 10
US-10-108-260A-4725
; Sequence 4725, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4725
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-108-260A-4725

Query Match 47.2%; Score 154; DB 15; Length 109;
Best Local Similarity 81.1%; Pred. No. 7.3e-13;
Matches 30; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 6 VAQAGVQPHDLGSLQSLPRFKRFSCLILPKIWDYRN 42
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 29 VAQAGVQPHDLGSLQSLPRFKRFSCLSLPGSGWDYRH 65

RESULT 11

US-10-104-047-2423
; Sequence 2423, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2423
; LENGTH: 114
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-104-047-2423

Query Match 45.6%; Score 148.5; DB 15; Length 114;
Best Local Similarity 54.2%; Pred. No. 4.3e-12;
Matches 32; Conservative 5; Mismatches 17; Indels 5; Gaps 1;

QY 2 EPHTVAGVQPHDLGSLQSLPRFKRFSCLILPKIWDYRN-----NTALIKNRYTP 55
|| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 14 EPRPVAQAGVQWHNLGSRQLPPRFRKFSCLSLSSWDYRHPHPANFCIFSRDGVSP 72

RESULT 12

US-10-104-047-3765
; Sequence 3765, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3765
; LENGTH: 104
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-104-047-3765

Query Match 45.1%; Score 147; DB 15; Length 104;
Best Local Similarity 73.2%; Pred. No. 6.3e-12;
Matches 30; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 MESHVAQAGVQWCDLGLSLQSLPRFKRFSCLILPKIWDYR 41
|| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MESHVAQAGVQWCDLGLSLQSLPRFKRFSCLSLPGSGWDYR 41

RESULT 13

US-10-017-161-1210
; Sequence 1210, Application US/10017161
; Publication No. US20030143668A1

; GENERAL INFORMATION:

; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1210
; LENGTH: 151
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-017-161-1210

Query Match 45.1%; Score 147; DB 14; Length 151;
Best Local Similarity 69.0%; Pred. No. 9.6e-12;
Matches 29; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 2 EPHTVAGVQPHDLGSLQSLPRFKRFSCLILPKIWDYRN 43
|| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 50 ESHVAQAGVQWRDLGSLQSLPPRFRKFSCLSLPSNWDYRHV 91

RESULT 14

US-10-292-798-1020
; Sequence 1020, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1020
; LENGTH: 151
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-292-798-1020

Query Match 45.1%; Score 147; DB 15; Length 151;
Best Local Similarity 69.0%; Pred. No. 9.6e-12;
Matches 29; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 2 EPHTVAGVQPHDLGSLQSLPRFKRFSCLILPKIWDYRN 43
|| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 50 ESHVAQAGVQWRDLGSLQSLPPRFRKFSCLSLPSNWDYRHV 91

RESULT 15

US-10-006-867-134
; Sequence 134, Application US/10006867
; Publication No. US20020119130A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

; PRIOR APPLICATION NUMBER: 60/114223
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/115614
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116527
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/119285
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/119287
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/119525
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/120014
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/129122
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/129674
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/138387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/175481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/191007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/199397
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/380139
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380142

Query Match 42.9%; Score 140; DB 13; Length 440;
Best Local Similarity 52.6%; Pred. No. 3e-10;
Matches 30; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Qy 2 EPHTVAGVPOHDLGSLQSLPRFKRFSCLILPKIWDYRNMNTALIKRNRYPETG 58
Db 357 DSRSAQAGVQWRNLGSLQPLPGFKQFSCLILPSSWDYRSPPYLANFYFLVETG 413

Search completed: October 11, 2005, 07:39:48
Job time : 103.265 secs

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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:19 ; Search time 13.9452 Seconds
(without alignments)
326.535 Million cell updates/sec

Title: US-10-092-934-9
Perfect score: 326
Sequence: 1 MEHPTVAQGVPOHDLGSLQ.....NMNTALIKRNYRPTGGRKS 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	140	42.9	54	4	US-09-513-999C-7519
2	135	41.4	63	4	US-09-621-976-4553
3	133	40.8	61	4	US-09-513-999C-4581
4	132.5	40.6	397	5	PCT-US95-17111A-121
5	131	40.2	103	4	US-09-513-999C-5327
6	130.5	40.0	375	2	US-08-454-557C-121
7	130.5	40.0	375	2	US-08-340-426D-121
8	130.5	40.0	375	2	US-08-450-673C-121
9	130.5	40.0	375	4	US-09-872-968-2
10	128	39.3	64	4	US-09-513-999C-4425
11	126	38.7	64	4	US-09-513-999C-6611
12	124.5	38.2	68	4	US-09-621-976-6572
13	124	38.0	96	4	US-09-513-999C-6065
14	124	38.0	120	4	US-09-621-976-5592
15	124	38.0	132	4	US-09-636-215-573
16	124	38.0	132	4	US-09-685-166A-573
17	124	38.0	132	4	US-09-679-426-573
18	124	38.0	132	4	US-09-759-143-573
19	124	38.0	132	4	US-09-651-236-573
20	124	38.0	135	4	US-09-685-166A-884
21	124	38.0	135	4	US-09-679-426-884
22	124	38.0	135	4	US-09-759-143-884
23	124	38.0	776	4	US-10-020-079-24
24	124	38.0	789	4	US-10-020-079-22
25	124	38.0	863	4	US-10-020-079-32
26	124	38.0	876	4	US-10-020-079-30
27	124	38.0	889	4	US-10-020-079-20

28	124	38.0	895	4	US-10-020-079-18	Sequence 18, Appl
29	124	38.0	976	4	US-10-020-079-28	Sequence 28, Appl
30	124	38.0	982	4	US-10-020-079-26	Sequence 26, Appl
31	123	37.7	63	4	US-09-621-976-6005	Sequence 6005, Ap
32	123	37.7	76	4	US-09-621-976-6338	Sequence 6338, Ap
33	123	37.7	90	4	US-09-621-976-4397	Sequence 4397, Ap
34	122.5	37.6	108	4	US-09-513-999C-7878	Sequence 7878, Ap
35	121	37.1	54	4	US-09-513-999C-7068	Sequence 7068, Ap
36	118	36.2	87	4	US-09-621-976-4482	Sequence 4482, Ap
37	117	35.9	121	4	US-09-513-999C-7874	Sequence 7874, Ap
38	115.5	35.4	91	4	US-09-621-976-5929	Sequence 5929, Ap
39	115	35.3	66	4	US-09-621-976-5606	Sequence 5606, Ap
40	115	35.3	87	4	US-09-205-258-342	Sequence 342, App
41	115	35.3	111	4	US-09-513-999C-8159	Sequence 8159, Ap
42	114.5	35.1	119	4	US-09-513-999C-7867	Sequence 7867, Ap
43	114	35.0	65	4	US-09-513-999C-6665	Sequence 6665, Ap
44	114	35.0	70	4	US-09-513-999C-6561	Sequence 6561, Ap
45	114	35.0	118	4	US-09-663-600A-114	Sequence 114, App

ALIGNMENTS

RESULT 1
US-09-513-999C-7519
; Sequence 7519, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7519
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-7519

Query Match	42.9%	Score 140;	DB 4;	Length 54;
Best Local Similarity	65.9%	Pred. No. 4.2e-13;		
Matches	27;	Conservative	4;	Mismatches 10; Indels 0; Gaps 0;
Oy	1	MEHPTVAQGVPOHDLGSLQSLPRKFRFSCLLIPKIDYR	41	
Db	12	MESRLAQAGLQWHLGSLQPLPPGFRFRFSCLSLPSSWDYR	52	

RESULT 2
US-09-621-976-4553
; Sequence 4553, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4553
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-621-976-4553

Query Match 41.4%; Score 135; DB 4; Length 63;
Best Local Similarity 70.7%; Pred. No. 2.7e-12;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 MEPTVAQAGVPQHDIGSLQSLPRPKRFSCILIPK1WDYR 41
Db 15 MESCVAQAGVRVCHLGSLOPLPPPKRFSCILIPSSWDYR 55

RESULT 3

US-09-513-999C-4581
; Sequence 4581, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4581
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -16..-1
; OTHER INFORMATION: score 7.5
; OTHER INFORMATION: seq LFCLSVCLFEVES/HS
US-09-513-999C-4581

Query Match 40.8%; Score 133; DB 4; Length 61;
Best Local Similarity 61.9%; Pred. No. 5.2e-12;
Matches 26; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 1 MEPTVAQAGVPQHDIGSLQSLPRPKRFSCILIPK1WDYR 42
Db 14 VESHVTQAGVQVHSLGPLNSLPPGPKRFSCILSSSDYRH 55

RESULT 4

PCT-US95-17111A-121
; Sequence 121, Application PC/TUS9517111A
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
; TITLE OF INVENTION: Detection of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17111A
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,426
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-17111A-121

Query Match 40.6%; Score 132.5; DB 5; Length 397;
Best Local Similarity 59.2%; Pred. No. 6.4e-11;
Matches 29; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

QY 1 MEPTVAQAGVPQHDIGSLQSLPRPKRFSCILIPK1WDYRNM-NTALI 48
Db 305 MESHVTQAGVQVNPGLSLQPLPPGPKRFSCILPSSWDYGHLLHTPLI 353

RESULT 5

US-09-513-999C-5327
; Sequence 5327, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5327
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 78
; OTHER INFORMATION: Xaa=His or Gln
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 88
; OTHER INFORMATION: Xaa=Lys or Asn or Arg or Ser
US-09-513-999C-5327

Query Match 40.2%; Score 131; DB 4; Length 103;
Best Local Similarity 70.3%; Pred. No. 2e-11;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 5 TVAQAGVPQHDIGSLQSLPRPKRFSCILIPK1WDYR 41
Db 6 SVTQAGVQVHDLGSLOPLPPGPKRFSCILPSSWDYR 42

RESULT 6

US-08-454-557C-121
; Sequence 121, Application US/08454557C
; Patent No. 5830670
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne


```
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,557C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-454-557C-121

Query Match 40.0%; Score 130.5; DB 2; Length 375;
Best Local Similarity 48.3%; Pred. No. 1.2e-10;
Matches 29; Conservative 6; Mismatches 20; Indels 5; Gaps 1;

QY 1 MEHPTVAQGVQPHDLGSLQSLPRFRKFSCLILPKIWDYRNM-----NTALIKRNYTP 55
Db 304 MESHVTOAGVQVWPNLGSLOPLPGLKRFSCSLSPSSWDYGHLPHPANFCIFIRGGVSP 363

RESULT 7
US-08-340-426D-121
; Sequence 121, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,426D
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
```

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; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-340-426D-121

Query Match 40.0%; Score 130.5; DB 2; Length 375;
Best Local Similarity 48.3%; Pred. No. 1.2e-10;
Matches 29; Conservative 6; Mismatches 20; Indels 5; Gaps 1;

QY 1 MEHPTVAQGVQPHDLGSLQSLPRFRKFSCLILPKIWDYRNM-----NTALIKRNYTP 55
Db 304 MESHVTOAGVQVWPNLGSLOPLPGLKRFSCSLSPSSWDYGHLPHPANFCIFIRGGVSP 363

RESULT 8
US-08-450-673C-121
; Sequence 121, Application US/08450673C
; Patent No. 5948888
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,673C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-450-673C-121

Query Match 40.0%; Score 130.5; DB 2; Length 375;
Best Local Similarity 48.3%; Pred. No. 1.2e-10;
Matches 29; Conservative 6; Mismatches 20; Indels 5; Gaps 1;

QY 1 MEHPTVAQGVQPHDLGSLQSLPRFRKFSCLILPKIWDYRNM-----NTALIKRNYTP 55
Db 304 MESHVTOAGVQVWPNLGSLOPLPGLKRFSCSLSPSSWDYGHLPHPANFCIFIRGGVSP 363

RESULT 9
US-09-872-968-2
```

; Sequence 2, Application US/09872968
; Patent No. 6770797
; GENERAL INFORMATION:
; APPLICANT: wands, Jack R
; APPLICANT: de la Monte, Suzanne M
; TITLE OF INVENTION: Inhibition of Neurodegeneration
; FILE REFERENCE: 21486-047
; CURRENT APPLICATION NUMBER: US/09/872,968
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-968-2

Query Match 40.0%; Score 130.5; DB 4; Length 375;
Best Local Similarity 48.3%; Pred. No. 1.2e-10;
Matches 29; Conservative 6; Mismatches 20; Indels 5; Gaps 1;
QY 1 MEPHTVAQGVPOHDLGSLQSLPRKRFSCILIPKIDYRNM-----NTALIKRNYTP 55
Db 304 MESHVTAQGVQWPNLGLSLQPLPGLKRFSCILPSSWDYGHLPHPANPCIFIRGVSP 363

RESULT 10
US-09-513-999C-4425
; Sequence 4425, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4425
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -14..-1
; OTHER INFORMATION: score 4.4
; OTHER INFORMATION: seq HIFLSPFIETDS/HS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 10
; OTHER INFORMATION: Xaa= * or Trp
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 29
; OTHER INFORMATION: Xaa=Leu or Val
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 41
; OTHER INFORMATION: Xaa=Pro or Ser
US-09-513-999C-4425

Query Match 39.3%; Score 128; DB 4; Length 64;
Best Local Similarity 62.5%; Pred. No. 3e-11;
Matches 25; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 2 EPHTVAGVPOHDLGSLQSLPRKRFSCILIPKIDYR 41
Db 13 DSHSVAQGVQVRDLGSLQAPLPGFTTFSCXSLPSSWDYR 52

RESULT 11
US-09-513-999C-6611
; Sequence 6611, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6611
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6611

Query Match 38.7%; Score 126; DB 4; Length 64;
Best Local Similarity 64.1%; Pred. No. 5.8e-11;
Matches 25; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 MEPHTVAQGVPOHDLGSLQSLPRKRFSCILIPKID 39
Db 1 MGSHSVTAQDMQLHDLGSLQPLPRKQFSRLSLPRSD 39

RESULT 12
US-09-621-976-6572
; Sequence 6572, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6572
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 29
; OTHER INFORMATION: Xaa = His,Asn
US-09-621-976-6572

Query Match 38.2%; Score 124.5; DB 4; Length 68;
Best Local Similarity 61.4%; Pred. No. 1e-10;
Matches 27; Conservative 4; Mismatches 10; Indels 3; Gaps 1;

QY 1 MEPHTVA---QAGVPOHDLGSLQSLPRKRFSCILIPKIDYR 41
Db 12 VEPWSLALLPEAGVRWCXIGSLQPLPRKRFSCILPSSWDYR 55

RESULT 13
US-09-513-999C-6065
; Sequence 6065, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.

```
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59,US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6065
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6065

Query Match      38.0%; Score 124; DB 4; Length 96;
Best Local Similarity 65.8%; Pred. No. 1.9e-10;
Matches 25; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 6 VAQAGVQPHDLGSLQSLPRFKRFSCLILPKIWDYRNM 43
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6 VAQAGVQWRDLGSPQPLPPGFKRFSCLSPSSWDYRHV 43
      ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-09-621-976-5592
; Sequence 5592, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5592
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -105...-1
US-09-621-976-5592

Query Match      38.0%; Score 124; DB 4; Length 120;
Best Local Similarity 41.9%; Pred. No. 2.5e-10;
Matches 31; Conservative 8; Mismatches 19; Indels 16; Gaps 3;

QY 3 PHTVAQ-----AGVPQHDLSLQSLPRFKRFSCLILPKIWDYRN-----MNTAL 47
      ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 9 PEVIAQLENAAKVLMAGVQWHDLSLQSLPRFKRFSCLSPSSWDYRHHLPMWIMNNAS 68
      ||| ||||| ||||| ||||| ||||| ||||| |||||

QY 48 IKRNYTPETGRKS 61
      : : : : :
Db 69 M-QSTYSYHLGNQN 81

RESULT 15
US-09-636-215-573
; Sequence 573, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
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; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.4217CI7
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 573
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-215-573

Query Match      38.0%; Score 124; DB 4; Length 132;
Best Local Similarity 65.0%; Pred. No. 2.9e-10;
Matches 26; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 2 EPHTVAQAGVPQHDLSLQSLPRFKRFSCLILPKIWDYR 41
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 34 ESGFVAQAGVQWHDLSLQSLPRFKRFSCLSPSSWDHR 73
      ||||| ||||| ||||| ||||| ||||| ||||| |||||

Search completed: October 11, 2005, 07:42:52
Job time : 13.9452 secs
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